

Sequences producing significant alignments:

Peptide

Score (bits) E Value

gi 22416427 gb AAM96215.1	potassium-chloride transporter-3...	1226	0.0	G
gi 6693798 gb AAF24986.1	K-Cl cotransporter KCC3 [Homo sap...	1226	0.0	G
gi 33329252 gb AAQ10026.1	K-Cl cotransporter KCC3a-X2M iso...	1208	0.0	G
gi 41281645 ref NP_598410.1	solute carrier family 12, memb...	1197	0.0	G
gi 47124056 gb AAH70107.1	SLC12A6 protein [Homo sapiens]	1184	0.0	G
gi 33329256 gb AAQ10028.1	K-Cl cotransporter KCC3a-S2 isof...	1183	0.0	G
gi 38565928 gb AAH62099.1	Unknown (protein for MGC:69652) ...	1157	0.0	
gi 22416428 gb AAM96216.1	potassium-chloride transporter-3...	1154	0.0	G
gi 19526769 ref NP_598409.1	solute carrier family 12, memb...	1134	0.0	G
gi 34856648 ref XP_342490.1	similar to K-Cl cotransporter ...	1117	0.0	G
gi 7512561 pir T17275	hypothetical protein DKFZp434D2135.1...	1116	0.0	G
gi 19110891 gb AAL85335.1	K-Cl cotransporter KCC3 variant ...	1115	0.0	G
gi 9507107 ref NP_062102.1	solute carrier family 12, membe...	865	0.0	G
gi 45219767 gb AAH66872.1	Solute carrier family 12, member...	862	0.0	G
gi 27151684 sp Q28677 S124	RABIT Solute carrier family 12 m...	862	0.0	
gi 6677993 ref NP_033221.1	solute carrier family 12, membe...	862	0.0	G

gi 4827006 ref NP_005063.1 	solute carrier family 12 (potas...	862	0.0	
gi 47213488 emb CAF91145.1 	unnamed protein product [Tetrao...	859	0.0	
gi 31324218 gb AAP47188.1 	potassium-chloride cotransporter...	856	0.0	
gi 47522728 ref NP_999114.1 	K-Cl cotransporter [Sus scrofa...	856	0.0	
gi 3015641 gb AAC39685.1 	erythroid K:Cl cotransporter spli...	837	0.0	
gi 11968148 ref NP_065759.1 	solute carrier family 12 membe...	783	0.0	
gi 19705463 ref NP_599190.1 	solute carrier family 12 membe...	783	0.0	
gi 12003227 gb AAG43493.1 	electroneutral potassium-chlorid...	783	0.0	
gi 14193696 gb AAK56093.1 	K-Cl cotransporter [Mus musculus...	780	0.0	
gi 28972652 dbj BAC65742.1 	mKIAA1176 protein [Mus musculus]	780	0.0	
gi 3015639 gb AAC39684.1 	erythroid K:Cl cotransporter spli...	780	0.0	
gi 33859680 ref NP_065066.1 	solute carrier family 12, memb...	778	0.0	
gi 6755534 ref NP_035520.1 	solute carrier family 12, membe...	773	0.0	
gi 47847414 dbj BAD21379.1 	mFLJ00098 protein [Mus musculus]	773	0.0	
gi 6330233 dbj BAA86490.1 	KIAA1176 protein [Homo sapiens]	772	0.0	
gi 5730043 ref NP_006589.1 	solute carrier family 12 (potas...	767	0.0	
gi 50753670 ref XP_414082.1 	PREDICTED: similar to K-Cl cot...	766	0.0	
gi 50733496 ref XP_418891.1 	PREDICTED: similar to mFLJ0009...	761	0.0	
gi 32490535 gb AAP84988.1 	potassium-chloride cotransporter...	753	0.0	
gi 47225214 emb CAF98841.1 	unnamed protein product [Tetrao...	753	0.0	
gi 9651224 gb AAF91094.1 	K-Cl cotransporter KCC1 [Mus musc...	707	0.0	
gi 47223173 emb CAG11308.1 	unnamed protein product [Tetrao...	688	0.0	
gi 47220725 emb CAG11794.1 	unnamed protein product [Tetrao...	687	0.0	
gi 47213000 emb CAF95392.1 	unnamed protein product [Tetrao...	672	0.0	
gi 24762439 ref NP_726378.1 	CG5594-PA [Drosophila melanoga...	598	e-169	
gi 21429886 gb AAM50621.1 	GH09271p [Drosophila melanogaste...	597	e-169	
gi 46409210 gb AAS93762.1 	LD02554p [Drosophila melanogaste...	595	e-168	
gi 22026947 ref NP_571976.2 	CG5594-PC [Drosophila melanoga...	594	e-168	
gi 10440500 dbj BAB15783.1 	FLJ00098 protein [Homo sapiens]	531	e-149	
gi 48096020 ref XP_394587.1 	similar to CG5594-PC [Apis mel...	531	e-149	
gi 10440514 dbj BAB15787.1 	FLJ00105 protein [Homo sapiens]	501	e-140	
gi 34853395 ref XP_217744.2 	similar to putative potassium-...	452	e-125	
gi 25149428 ref NP_500910.2 	solute carrier family 12 membe...	440	e-121	
gi 39584234 emb CAE61609.1 	Hypothetical protein CBG05529 [...	438	e-121	
gi 31226974 ref XP_317803.1 	ENSANGP00000014479 [Anopheles ...	420	e-115	
gi 17541928 ref NP_501141.1 	solute carrier family 12 membe...	360	2e-97	
gi 39593544 emb CAE61836.1 	Hypothetical protein CBG05808 [...	353	2e-95	
gi 26343083 dbj BAC35198.1 	unnamed protein product [Mus mu...	332	3e-89	
gi 18073139 emb CAC80545.1 	putative Na-K-Cl cotransporter ...	322	4e-86	
gi 39596034 emb CAE67537.1 	Hypothetical protein CBG13060 [...	320	1e-85	
gi 31226957 ref XP_317800.1 	ENSANGP00000004794 [Anopheles ...	311	8e-83	
gi 13507237 gb AAK28520.1 	K-Cl cotransporter [Xenopus laevis]	309	3e-82	
gi 17534831 ref NP_495555.1 	Na-K-Cl cotransporter (2H716) ...	299	3e-79	
gi 32484273 gb AAH54325.1 	LOC398663 protein [Xenopus laevis]	224	8e-57	
gi 31226979 ref XP_317804.1 	ENSANGP00000024771 [Anopheles ...	208	8e-52	
gi 50944163 ref XP_481609.1 	putative Na+/K+/Cl-transport...	206	4e-51	
gi 15208177 dbj BAB63113.1 	hypothetical protein [Macaca fa...	202	4e-50	
gi 2582381 gb AAC49874.1 	cation-chloride co-transporter [N...	201	1e-49	
gi 9651629 gb AAF91220.1 	potassium-chloride cotransporter ...	200	2e-49	

<u>gi 47193414 emb CAG14039.1 </u>	unnamed protein product [Tetrao...	194	2e-47	
<u>gi 30691724 ref NP_849732.1 </u>	cation-chloride cotransporter,...	194	2e-47	G
<u>gi 6634764 gb AAF19744.1 </u>	Strong similarity to gb AF021220 ...	192	4e-47	
<u>gi 47203569 emb CAG13773.1 </u>	unnamed protein product [Tetrao...	187	1e-45	
<u>gi 3582769 gb AAC35282.1 </u>	erythrocyte K-Cl cotransporter [H...	183	3e-44	G
<u>gi 9651216 gb AAF91090.1 </u>	K-Cl cotransporter [Mus musculus]	165	6e-39	G
<u>gi 3925714 emb CAA09464.1 </u>	KCC2 protein [Mus musculus]	153	3e-35	G
<u>gi 14043556 gb AAH07760.1 </u>	SLC12A7 protein [Homo sapiens]	149	6e-34	G
<u>gi 35505532 gb AAH57624.1 </u>	Slc12a5 protein [Mus musculus]	147	2e-33	G
<u>gi 31226967 ref XP_317802.1 </u>	ENSANGP00000015001 [Anopheles ...	141	9e-32	G
<u>gi 7512576 pir T17231</u>	hypothetical protein DKFZp434F076.1 ...	136	4e-30	G
<u>gi 20151457 gb AAM11088.1 </u>	GH27027p [Drosophila melanogaste...	133	3e-29	G
<u>gi 52075682 dbj BAD44902.1 </u>	putative potassium-chloride cot...	130	2e-28	
<u>gi 38073246 gb AAR10807.1 </u>	K-Cl cotransporter KCC3a isoform...	130	3e-28	
<u>gi 50778569 ref XP_427392.1 </u>	PREDICTED: similar to solute c...	127	2e-27	G
<u>gi 48119195 ref XP_393214.1 </u>	similar to bumetanide sensitiv...	123	3e-26	G
<u>gi 34905658 ref NP_914176.1 </u>	putative cation-chloride co-tr...	121	1e-25	G
<u>gi 1673531 gb AAB18960.1 </u>	furosemide-sensitive K-Cl cotrans...	120	2e-25	
<u>gi 38073248 gb AAR10808.1 </u>	brain-specific K-Cl cotransporte...	111	1e-22	
<u>gi 31236589 ref XP_319440.1 </u>	ENSANGP00000014326 [Anopheles ...	111	1e-22	G
<u>gi 13937397 ref NP_113583.1 </u>	solute carrier family 12 (potass...	106	4e-21	G
<u>gi 51859114 gb AAH81728.1 </u>	Cation-chloride cotransporter 6 ...	105	9e-21	G
<u>gi 13516498 dbj BAB40456.1 </u>	cation chloride cotransporter 6...	105	9e-21	G
<u>gi 51094566 gb EAL23818.1 </u>	solute carrier family 12 (potass...	104	2e-20	G
<u>gi 9502260 gb AAF88060.1 </u>	cation-chloride cotransporter-int...	103	2e-20	G
<u>gi 6179898 gb AAF05702.1 </u>	Na+/K+/2Cl- cotransporter [Callin...	101	1e-19	
<u>gi 14486416 gb AAK62044.1 </u>	Na+/K+/2Cl- cotransporter [Carc...	101	1e-19	
<u>gi 48101446 ref XP_395129.1 </u>	similar to ENSANGP00000014326 ...	100	2e-19	G
<u>gi 13383504 gb AAK21009.1 </u>	cation-chloride cotransporter-in...	100	2e-19	
<u>gi 50423949 ref XP_460559.1 </u>	unnamed protein product [Debar...	100	3e-19	G
<u>gi 31242251 ref XP_321556.1 </u>	ENSANGP00000011560 [Anopheles ...	100	4e-19	G
<u>gi 19705533 ref NP_599232.1 </u>	cation-chloride cotransporter ...	99	5e-19	G
<u>gi 25304083 gb AAH40138.1 </u>	Unknown (protein for MGC:48843) ...	98	1e-18	
<u>gi 516001 gb AAC48592.1 </u>	bumetanide-sensitive Na-K-Cl contra...	97	2e-18	
<u>gi 1709296 sp P55015 S121_RABIT</u>	Solute carrier family 12 me...	97	3e-18	
<u>gi 9507103 ref NP_062007.1 </u>	solute carrier family 12, membe...	97	3e-18	G
<u>gi 4557849 ref NP_000329.1 </u>	sodium potassium chloride contra...	97	3e-18	G
<u>gi 1079521 gb AAC52633.1 </u>	kidney-specific Na-K-Cl cotranspo...	97	3e-18	G
<u>gi 2290526 gb AAB65150.1 </u>	Na-(K)-Cl cotransporter isoform m...	97	3e-18	G
<u>gi 6755532 ref NP_035519.1 </u>	solute carrier family 12, membe...	96	7e-18	G
<u>gi 34365781 ref NP_899197.1 </u>	solute carrier family 12, memb...	96	7e-18	G
<u>gi 16877251 gb AAH16888.1 </u>	Solute carrier family 12, member...	96	7e-18	G
<u>gi 27151793 sp P55014 S121_MOUSE</u>	Solute carrier family 12 m...	96	7e-18	G
<u>gi 40950187 gb AAR97733.1 </u>	Na-K-Cl cotransporter [Oreochrom...	96	7e-18	
<u>gi 17543066 ref NP_502704.1 </u>	solute carrier family 12 membe...	95	1e-17	G
<u>gi 47230656 emb CAF99849.1 </u>	unnamed protein product [Tetrao...	95	1e-17	
<u>gi 21483278 gb AAM52614.1 </u>	GH09711p [Drosophila melanogaste...	95	1e-17	G
<u>gi 20177071 gb AAM12297.1 </u>	RH37201p [Drosophila melanogaster]	95	1e-17	
<u>gi 24644255 ref NP_730939.1 </u>	CG31547-PA [Drosophila melanog...	95	1e-17	G

gi 39586961 emb CAE62896.1	Hypothetical protein CBG07084 [...	94	3e-17	
gi 2136942 pir I46497	bumetanide-sensitive Na-K-Cl cotrans...	93	5e-17	
gi 27652641 emb CAD31111.1	putative sodium-potassium-chlor...	93	5e-17	
gi 2137580 pir I49269	Na+/K+/Cl-cotransport protein renal ...	93	5e-17	G
gi 47224809 emb CAG06379.1	unnamed protein product [Tetrao...	92	1e-16	
gi 50752967 ref XP_413814.1	PREDICTED: similar to bumetani...	91	1e-16	G
gi 15010508 gb AAK77302.1	GH08340p [Drosophila melanogaste...	91	2e-16	G
gi 31197669 ref XP_307782.1	ENSANGP00000012928 [Anopheles ...	91	2e-16	G
gi 23955920 gb AAN40689.1	putative sodium-potassium-2-chlo...	91	2e-16	
gi 47227672 emb CAG09669.1	unnamed protein product [Tetrao...	91	2e-16	
gi 40950185 gb AAR97732.1	Na-K-Cl cotransporter [Oreochrom...	91	2e-16	
gi 47210716 emb CAF92943.1	unnamed protein product [Tetrao...	90	4e-16	
gi 27652643 emb CAD31112.1	putative sodium-potassium-chlor...	89	5e-16	
gi 40950183 gb AAR97731.1	Na-K-Cl cotransporter [Oreochrom...	89	5e-16	
gi 21686589 gb AAM74968.1	renal Na-K-Cl cotransporter isof...	89	7e-16	
gi 21686587 gb AAM74967.1	renal Na-K-Cl cotransporter isof...	89	7e-16	
gi 47213642 emb CAF90346.1	unnamed protein product [Tetrao...	89	9e-16	
gi 596076 gb AAA75600.1	bumetanide sensitive NaK2Cl cotran...	88	1e-15	
gi 17535967 ref NP_493773.1	cation-chloride cotransporter-...	88	2e-15	G
gi 50727039 gb AAT81190.1	Hypothetical protein T04B8.5b [C...	88	2e-15	
gi 50344814 ref NP_001002080.1	zgc:85961 [Danio rerio] >gi...	88	2e-15	G
gi 4506977 ref NP_000330.1	solute carrier family 12 (sodiu...	87	3e-15	G
gi 1717801 sp P55017 S123_HUMAN	Solute carrier family 12 me...	87	3e-15	G
gi 7513175 pir G01202	NaCl electroneutral Thiazide-sensiti...	87	3e-15	G
gi 5759119 gb AAD50984.1	Na-K-2Cl- cotransporter [Oryctola...	87	3e-15	
gi 1083802 pir B54145	sodium-chloride transporter, Thiazid...	86	4e-15	
gi 33563368 ref NP_062218.2	solute carrier family 12, memb...	86	4e-15	G
gi 21686585 gb AAM74966.1	renal Na-K-Cl cotransporter isof...	86	6e-15	
gi 21686583 gb AAM74965.1	renal Na-K-Cl cotransporter isof...	86	6e-15	
gi 2599070 gb AAC33139.1	thiazide-sensitive sodium chlorid...	86	6e-15	
gi 2136267 pir PC4180	thiazide-sensitive sodium-chloride c...	86	8e-15	
gi 38073244 gb AAR10806.1	K-Cl cotransporter KCC3b isoform...	85	1e-14	
gi 14547897 ref NP_062288.1	solute carrier family 12, memb...	85	1e-14	G
gi 24047306 gb AAH38612.1	Solute carrier family 12, member...	85	1e-14	G
gi 30721813 gb AAP33906.1	bumetanide-sensitive Na-K-Cl cot...	84	2e-14	G
gi 6677991 ref NP_033220.1	solute carrier family 12, membe...	84	2e-14	G
gi 2147143 pir I51307	basolateral Na(+)-K(+)-Cl- cotranspo...	84	2e-14	
gi 1709294 sp P55013 S122_SQUAC	Solute carrier family 12 me...	84	3e-14	
gi 34879509 ref XP_346514.1	hypothetical protein XP_346513...	84	3e-14	G
gi 27807511 ref NP_777207.1	solute carrier family 12 (sodi...	84	3e-14	G
gi 13929130 ref NP_113986.1	solute carrier family 12, memb...	84	3e-14	G
gi 50761390 ref XP_424716.1	PREDICTED: similar to Solute c...	84	3e-14	G
gi 5081312 gb AAD39342.1	bumetanide-sensitive Na-K-2Cl cot...	84	3e-14	G
gi 47222533 emb CAG02898.1	unnamed protein product [Tetrao...	83	4e-14	
gi 50753599 ref XP_414059.1	PREDICTED: similar to solute c...	83	5e-14	G
gi 48102011 ref XP_392732.1	similar to CG4357-PA [Apis mel...	81	1e-13	G
gi 290856 gb AAA49272.1	thiazide sensitive NaCl cotranspor...	80	2e-13	
gi 1581614 prf 2117156A	basolateral Na/K/Cl cotransporter	80	2e-13	
gi 4584410 emb CAB40708.1	basolateral NaK(2Cl) cotransport...	78	2e-12	
gi 46441770 gb EAL01065.1	hypothetical protein Ca019.6833 ...	76	5e-12	
gi 34857570 ref XP_345417.1	similar to K-Cl cotransporter ...	75	8e-12	G
gi 21686581 gb AAM74964.1	renal Na-K-Cl cotransporter isof...	75	8e-12	
gi 21686579 gb AAM74963.1	renal Na-K-Cl cotransporter isof...	75	8e-12	

gi 46100179 gb EAK85412.1	hypothetical protein UM04602.1 [...]	74	2e-11	
gi 47226271 emb CAG09239.1	unnamed protein product [Tetrao...]	72	1e-10	
gi 37575103 gb AAQ93478.1	furosemide-sensitive KCl cotrans...	71	2e-10	
gi 46446456 ref YP_007821.1	putative bumetanide-sensitive ...	70	3e-10	G
gi 44984445 gb AAS53347.1	AFL025Cp [Eremothecium gossypii]...	70	3e-10	G
gi 50292197 ref XP_448531.1	unnamed protein product [Candi...]	70	3e-10	G
gi 6319712 ref NP_009794.1	Hypothetical ORF; Ybr235wp [Sac...]	70	4e-10	G
gi 50545908 ref XP_500492.1	hypothetical protein [Yarrowia...]	69	6e-10	G
gi 50311073 ref XP_455560.1	unnamed protein product [Kluyv...]	69	6e-10	G
gi 19112532 ref NP_595740.1	putative membrane transporter ...	69	7e-10	G
gi 45527020 ref ZP_00178221.1	COG0531: Amino acid transpor...	67	2e-09	
gi 17533079 ref NP_495469.1	cation-chloride cotransporter ...	67	4e-09	G
gi 48893479 ref ZP_00326715.1	COG0531: Amino acid transpor...	65	8e-09	
gi 32404944 ref XP_323085.1	hypothetical protein (AL5134...)	65	1e-08	G
gi 47013799 gb AAT08445.1	Na-K-Cl cotransporter isoform 2 ...	64	2e-08	
gi 38073242 gb AAR10805.1	K-Cl cotransporter KCC4 [Rattus ...]	64	2e-08	G
gi 24899633 ref NP_705889.1	cation-chloride cotransporter ...	64	2e-08	G
gi 23495278 dbj BAC20265.1	cation-chloride cotransporter 9...	64	2e-08	G
gi 19527414 ref NP_599012.1	solute carrier family 12, memb...	64	3e-08	G
gi 39582293 emb CAE67542.1	Hypothetical protein CBG13067 [...]	64	3e-08	
gi 21411274 gb AAH30926.1	Slc12a8 protein [Mus musculus]	63	4e-08	G
gi 20892349 ref XP_147174.1	cation-chloride cotransporter ...	63	4e-08	
gi 10440502 dbj BAB15784.1	FLJ00100 protein [Homo sapiens]	63	4e-08	G
gi 10440351 dbj BAB15711.1	FLJ00010 protein [Homo sapiens]	63	4e-08	G
gi 42551588 gb EAA74431.1	hypothetical protein FG05147.1 [...]	62	7e-08	G
gi 48140542 ref XP_397130.1	similar to CG12773-PA [Apis me...]	62	1e-07	G
gi 20093291 ref NP_619366.1	Na-K-Cl cotransporter [Methano...]	61	2e-07	G
gi 47013797 gb AAT08444.1	Na-K-Cl cotransporter isoform 1 ...	61	2e-07	
gi 45523845 ref ZP_00175172.1	COG0531: Amino acid transpor...	61	2e-07	
gi 39581643 emb CAE71764.1	Hypothetical protein CBG18756 [...]	61	2e-07	
gi 16417791 gb AAL18853.1	potassium chloride cotransporter...	60	3e-07	
gi 47202516 emb CAF87431.1	unnamed protein product [Tetrao...]	60	3e-07	
gi 4185298 gb AAD09008.1	Na-K-2Cl cotransporter [Rattus no...]	60	3e-07	G
gi 16588876 gb AAL26926.1	thiazide-sensitive Na-Cl cotrans...	60	4e-07	
gi 12652805 gb AAH00154.1	SLC12A9 protein [Homo sapiens]	59	6e-07	G
gi 50750706 ref XP_422105.1	PREDICTED: similar to solute c...	59	6e-07	G
gi 38107570 gb EAA53722.1	hypothetical protein MG09472.4 [...]	59	6e-07	G
gi 37906389 gb AAP44496.1	Na-K-Cl cotransporter [Aedes aeg...]	59	6e-07	
gi 38569457 ref NP_078904.3	solute carrier family 12, memb...	59	8e-07	G
gi 21666316 gb AAM73657.1	solute carrier family 12 member ...	59	8e-07	G
gi 28628359 gb AAO49174.1	cation-chloride cotransporter 9 ...	59	8e-07	G
gi 47209879 emb CAF91324.1	unnamed protein product [Tetrao...]	59	1e-06	
gi 15281553 gb AAK94307.1	solute carrier family 12 member ...	57	2e-06	G
gi 51476920 emb CAH18426.1	hypothetical protein [Homo sapi...]	57	2e-06	
gi 31216859 ref XP_316315.1	ENSANGP00000020551 [Anopheles ...]	57	3e-06	G
gi 40741631 gb EAA60821.1	hypothetical protein AN4478.2 [A...	57	3e-06	G
gi 33589522 gb AAQ22528.1	LD15480p [Drosophila melanogaste...]	57	4e-06	G
gi 33327540 gb AAQ09093.1	SLC12A8 cation-chloride cotransp...	55	8e-06	G
gi 3127109 gb AAC16048.1	Na-K-Cl cotransporter BSC2 [Rattu...	52	7e-05	G

<u>gi 15789485 ref NP_279309.1 </u>	cationic amino acid transporter...	52	1e-04	
<u>gi 79644 pir S06903</u>	hypothetical protein 128 - Synechococc...	51	2e-04	
<u>gi 26342949 dbj BAC35131.1 </u>	unnamed protein product [Mus mu...	50	4e-04	
<u>gi 31321986 gb AAM48576.1 </u>	RHAG-2 [Takifugu rubripes]	50	5e-04	
<u>gi 21226632 ref NP_632554.1 </u>	Amino acid permease [Methanosa...	46	0.005	
<u>gi 26992100 gb AAN86742.1 </u>	Na-K-Cl cotransporter homolog [R...	46	0.005	
<u>gi 47216974 emb CAG04916.1 </u>	unnamed protein product [Tetrao...	45	0.011	
<u>gi 47201162 emb CAF87719.1 </u>	unnamed protein product [Tetrao...	45	0.011	
<u>gi 31874120 emb CAD97969.1 </u>	hypothetical protein [Homo sapi...	42	0.074	
<u>gi 6324649 ref NP_014718.1 </u>	t-SNARE that resides on the end...	42	0.096	
<u>gi 16903173 gb AAK01946.1 </u>	K-Cl cotransporter [Homo sapiens]	40	0.37	
<u>gi 4584408 emb CAB40707.1 </u>	apical Na(2Cl)K cotransporter [B...	39	0.62	
<u>gi 48840136 ref ZP_00297064.1 </u>	COG0531: Amino acid transpor...	39	0.81	
<u>gi 16801675 ref NP_471943.1 </u>	similar to amino acid transpor...	39	0.81	
<u>gi 15922144 ref NP_377813.1 </u>	442aa long conserved hypotheti...	37	3.1	
<u>gi 50753376 ref XP_413964.1 </u>	PREDICTED: similar to bumetani...	37	3.1	
<u>gi 14521274 ref NP_126749.1 </u>	hypothetical protein PAB0712 [...]	37	4.0	
<u>gi 46906258 ref YP_012647.1 </u>	membrane protein, putative [Li...	37	4.0	
<u>gi 45519701 ref ZP_00171252.1 </u>	COG2244: Membrane protein in...	37	4.0	
<u>gi 24374728 ref NP_718771.1 </u>	flagellar biosynthetic protein...	36	5.3	
<u>gi 33236849 gb AAP98936.1 </u>	putative transport permease [Chl...	36	5.3	
<u>gi 52009842 ref ZP_00337204.1 </u>	COG4177: ABC-type branched-c...	36	5.3	
<u>gi 48862094 ref ZP_00315992.1 </u>	COG0167: Dihydroorotate dehy...	36	6.9	
<u>gi 20089515 ref NP_615590.1 </u>	antigen [Methanoscarcina acetiv...	36	6.9	
<u>gi 45382387 ref NP_990203.1 </u>	SOCS box-containing WD protein...	36	6.9	
<u>gi 50411673 ref XP_457068.1 </u>	unnamed protein product [Debar...	36	6.9	
<u>gi 47095094 ref ZP_00232706.1 </u>	membrane protein, putative [...]	36	6.9	
<u>gi 20143912 ref NP_599027.1 </u>	WD SOCS-box protein 1 isoform ...	35	9.0	
<u>gi 18677720 ref NP_056441.6 </u>	WD SOCS-box protein 1 isoform ...	35	9.0	
<u>gi 22760676 dbj BAC11291.1 </u>	unnamed protein product [Homo s...	35	9.0	
<u>gi 47096061 ref ZP_00233662.1 </u>	amino acid permease family p...	35	9.0	
<u>gi 6563198 gb AAF17193.1 </u>	WSB-1 protein [Homo sapiens] >gi ...	35	9.0	

Alignments

[Get selected sequences](#) [Select all](#) [Deselect all](#)

>gi|22416427|gb|AAM96215.1| potassium-chloride transporter-3a [Homo sapiens]
gi|5106523|gb|AAD39742.1| K-Cl cotransporter KCC3a [Homo sapiens]
gi|27151690|sp|Q9UHW9|S126_HUMAN Solute carrier family 12 member 6 (Electroneut
 cotransporter 3) (K-Cl cotransporter 3)
 Length = 1150

Score = 1226 bits (3173), Expect = 0.0

Identities = 835/1350 (61%), Positives = 842/1350 (62%), Gaps = 395/1350 (29%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLXXXXXXXXXXXXXXXXXXXXXXXTSRXXXX 60
 MHPPETTTKMASVRFMVTPTKIDDIPGL
 TSR
 Sbjct: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDLSSRSSRVFSSRESPETSRS--- 57

Query: 61 XXXXXXXXXXXSQNSGHKKAEGDEYMDTRPGATTSLATVAL----RTSHPQDVIED---- 111
 E M GATTSLATVAL RTSHPQDVIED
 Sbjct: 58 -----EPMSEMSGATTSLATVALDPPSDRTSHPQDVIEDLSQN 95

Query: 112 -ITGEHSQQLDD----QRNAYLNNNSNYELFEEESFDKNLA-----KVSSLLNRMA 156
 ITGEHSQQLDD RNAYLNNNSNYE +E FDKNLA KVSSLLNRMA
 Sbjct: 96 SITGEHSQQLDDGHKKARNAYLNNNSNYEE-GDEYFDKNLALFEEEMDTRPKVSSLLNRMA 154

Query: 157 NY----QGAKEHEEAENITNLXXXXXXXXXXXXQMG----LQNIFGVTFMGVYILFLRL 207
 NY QGAKEHEEAENIT MG LQNIFGV ILFLRL
 Sbjct: 155 NYTNLNTQGAKEHEEAENITEGKKPTKTPQMGTFMGVYLPCLQNIIFGV----ILFLRL 208

Query: 208 LPCTWVVGTAGVLQAFIAVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISR ALGPYLG 267
 TWVVGTAGVLQAFIAVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISR ALGP
 Sbjct: 209 ---TWVVGTAGVLQAFIAVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISR ALGP--- 262

Query: 268 TTFEIFLVYEFGGAVGLCF----AAAMYILGAI----IVPRAAIFHSDDALKESAA 315
 EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDALKESAA
 Sbjct: 263 -----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDALKESAA 313

Query: 316 MLNNMRVYGTAFVLMLVVFFIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFAPPHP 375
 MLNNMRVYGTAFVLMLVVFFIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFAPPHP
 Sbjct: 314 MLNNMRVYGTAFVLMLVVFFIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFAPPHP 373

Query: 376 VCMLGNRTLSS--IDVCSKTKEINNMTRHVP SK-----NATCDECNSSYFVHN 421
 VCMLGNRTLSS IDVCSKTKEINNM T VPSK NATCDE YFVHN
 Sbjct: 374 VCMLGNRTLSSRHDVCSKTKEINNM T--VPSKLWGFFCNSSQFFNATCDE---YFVHN 427

Query: 422 NVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIE----KSSDVLGSLNHEYVLVDPSAK 477
 NV TSIQGIPGLASGIITENLWSNYLPKGEIIE KSSDVLGSLNHEYVLVD
 Sbjct: 428 NV---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLVD--- 480

Query: 478 ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTTILAILTSLWGFVYLSNV 537
 ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTTILAILTTS FVYLSNV
 Sbjct: 481 ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTTILAILTTS---FVYLSNV 535

Query: 538 VLFGACIEGVVLRDKFG-----VGTL SWP-----SFFSTCGAGDAVKGNLVPWV 581
 VLFGACIEGVVLRDKFG VGTL SWP SFFSTCGAG
 Sbjct: 536 VLFGACIEGVVLRDKFGDAVKGNL VVGTLSWPSPWVIVIGSFFSTCGAG----- 584

Query: 582 IVIGSLQSLDNIITGAPPFLRWALLRLQAIK-----VFGHSKANGEPT----- 626
 LQSL TGAP RLLQAIK VFGHSKANGEPT
 Sbjct: 585 -----LQSL---TGAP-----RLLQAIKDNII PFLRVFGHSKANGEPTWALLTA 627

Query: 627 -----GILIASLD-----FFLMCYLFTLLRLTAALVAPIAELILSMCALQ----- 666
 GILIASLD FFLMCYLF L CALQ
 Sbjct: 628 AIAELGILIASLDLVAPILSMFFLMCYLFVN L-----ACALQTLLRTPN 671

Query: 667 -----RYYHWALSF MGMTPNWVN LARPRPRFSICLALMF-----IVAMVIAGMIGAEK 714
 RYYHWALSF MGM SICLALMF IVAMVIAGM
 Sbjct: 672 WRPRFRYYHWALSF MGM-----SICLALMFISSSWYYAIVAMVIAGM---- 712

Query: 715 SSWYYAIYKXIEYQSLSPHTDEDEWGDGI---XXXXXXXXXXXXEEGP---KNWRPQXXX 768
 IYK IEYQ E EWGDGI EEGP KNWRPQ
 Sbjct: 713 -----IYKIEYQGA----EKEWGDGIRGLSLSAARFALLRLEEGPPHTKNWRPQOLLV 761

Query: 769 XXXXXX-----XXXTFASQLKG NFLHV KAGKGXTIVGSVIV-----GEALAAEQT 814
 TFASQL KAGKG TIVGSVIV GEALAAEQT
 Sbjct: 762 LLKLDDELHV KHPRLTFASQL-----KAGKGLTIVGSVIVGNFLEN YGEALAAEQT 814

Query: 815 KHVVACGLLENYLMEAEKVKGFCQL---AKLREGISH-----GGMKHNTVVLIQSMGW 864
 KH LMEAEKVKGFCQL AKLREGISH GGMKHNTVV MGW
 Sbjct: 815 KH-----LMEAEKVKGFCQLVVAKLREGISHLIQSCGLGGMKHNTVV---MGW 860

Query: 865 PNGWRQSERVTTDARAWKTFIGTVKNINIDLPFAAHLLVA---SFFPSNVEQFSEG-- 919
 PNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSNVEQFSEG
 Sbjct: 861 PNGWRQSE---DARAWKTFIGTVR----VTTAAHLALLVAKNISFFPSNVEQFSEGNI 911

Query: 920 -VWWIVHDGGMLML---LLKQHKVWRK-----TVAQLEDNSISCSIQMKATFLYHLRIE 969
 VWWIVHDGGMLML LLKQHKVWRK TVAQLEDNSI + ATFLYHLRIE
 Sbjct: 912 DVWWIVHDGGMLMLPFLLKQHKVWRKCSIRIFTVAQLEDNSIOMKKDL-ATFLYHLRIE 970

Query: 970 AEVRIFKDEVVRTLEMHDSDISAYTYERHMRLSKMMEQRSQLM-----TERDRIAQL 1022
 AEV + +EMHDSDISAYTYER + MMEQRSQLM TERDR AQL
 Sbjct: 971 AEVEV-----VEMHDSDISAYTYERTL---MMEQRSQLRHMRLSKTERDREAQL 1017

Query: 1023 VKDRNSMLRLTSIGSXXXXXXXXXXXXYMAQDLLHTAVYQEKVHM-----SRGQ 1073
 VKDRNSMLRLTSIGS T YQEKVHM SRGQ
 Sbjct: 1018 VKDRNSMLRLTSIGSDEDE-----ETETYQEKVHMTWTKDKYMASRGQ 1060

Query: 1074 KAKSMEGF---NMRPDQSNVRRM---KLNEVIVNKSHEAKLVLLNMPGPPRNPEGDEN 1125
 KAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNMPGPPRNPEGDEN
 Sbjct: 1061 KAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNMPGPPRNPEGDEN 1120

Query: 1126 YMELFLEVLTXXXXXXXXXXXXXXSEVITIYS 1155
 YMELFLEVLT SEVITIYS
 Sbjct: 1121 YMELFLEVLTTEGLERVLLVRRGGSEVITIYS 1150

>gi|6693798|gb|AAF24986.1| **G** K-Cl cotransporter KCC3 [Homo sapiens]
 Length = 1150

Score = 1226 bits (3173), Expect = 0.0
 Identities = 835/1350 (61%), Positives = 842/1350 (62%), Gaps = 395/1350 (29%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPLGLXXXXXXXXXXXXXXXXXXXXXXXSRXXXX 60
 MHPPETTTKMASVRFMVTPTKIDDIPLG TSR
 Sbjct: 1 MHPPETTTKMASVRFMVTPTKIDDIPLGSDTSPDLSSRSSSRVFSSRESVPETSRS--- 57

Query: 61 XXXXXXXXXLSQNSGHKKAEGDEYMDTRPGATTSLATVAL----RTSHPQDVIED--- 111
 E M GATTSLATVAL RTSHPQDVIED
 Sbjct: 58 -----EPMSEMSGATTSLATVALDPPSDRTSHPQDVIEDLSQN 95

Query: 112 -ITGEHSQQLDD---QRNAYLNNNSNYELFEEESFDKNLA-----KVSSLLNRMA 156
 ITGEHSQQLDD RNAYLNNNSNYE +E FDKNLA KVSSLLNRMA
 Sbjct: 96 SITGEHSQQLDDGHKKARNAYLNNNSNYEE-GDEYFDKNLALFEEEMDTRPKVSSLLNRMA 154

Query: 157 NY----QGAKEHEEAENITNLXXXXXXXXXXXXQMG----LQNIFGVTFMGVYILFLRL 207
 NY QGAKEHEEAENIT MG LQNIFGV ILFLRL
 Sbjct: 155 NYTNLTQGAKEHEEAENITEGKKPTKTPQMGTFMGVYLPCLQNIIFGV----ILFLRL 208

Query: 208 LPCTWVVGTAGVLQAFIAVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLG 267
 TWVVGTAGVLQAFIAVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP
 Sbjct: 209 ---TWVVGTAGVLQAFIAVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP--- 262

Query: 268 TTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDALKESAA 315
 EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDALKESAA
 Sbjct: 263 -----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDALKESAA 313

Query: 316 MLNNMRVYGTAFVLVLMVVFIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFAPPHPF 375
 MLNNMRVYGTAFVLVLMVVFIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFAPPHPF
 Sbjct: 314 MLNNMRVYGTAFVLVLMVVFIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFAPPHPF 373

Query: 376 VCMLGNRTLSS--IDVCSKTKEINNMTRHVP SK-----NATCDECNSSYFVHN 421
 VCMLGNRTLSS IDVCSKTKEINNM T VPSK NATCDE YFVHN
 Sbjct: 374 VCMLGNRTLSSRHIDVCSKTKEINNM T--VPSKLWGFFCNSSQFFNATCDE---YFVHN 427

Query: 422 NVQFFTSIQQGIPGLASGIITENLWSNYLPKGEIIE---KSSDVLGSLNHEYVLVDPSAK 477
 NV TSIQQGIPGLASGIITENLWSNYLPKGEIIE KSSDVLGSLNHEYVLVD
 Sbjct: 428 NV---TSIQQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLVD--- 480

Query: 478 ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTLAILTSLWGFFFVYLSNV 537
 ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTLAILTTS FVYLSNV
 Sbjct: 481 ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTLAILTTS---FVYLSNV 535

Query: 538 VLFGACIEGVVLRDKFG-----VGTL SWP-----SFFSTCGAGDAVKGNLVPWV 581
 VLFGACIEGVVLRDKFG VGTL SWP SFFSTCGAG
 Sbjct: 536 VLFGACIEGVVLRDKFGDAVKGNL VVGTLSWPSPWVIVIGSFFSTCGAG----- 584

Query: 582 IVIGSLQSLDNIITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT----- 626
 LQSL TGAP RLLQAIK VFGHSKANGEPT
 Sbjct: 585 ----LQSL---TGAP-----RLLQAIKDNII PFLRVFGHSKANGEPTWALLTA 627

Query: 627 ----GILIASLD-----FFLMCYLFTLLRLTAALVAPIAELILSMCALQ----- 666
 GILIASLD FFLMCYLF L CALQ
 Sbjct: 628 AIAELGILIASLDLVAPILSMFFFLMCYLFVN L-----ACALQTLLRTPN 671

Query: 667 ----RYYHWALSF MGMTPNWVN LARPRPRSICLALMF-----IVAMVIAGMIGAEK 714
 RYYHWALSF MGM SICLALMF IVAMVIAGM
 Sbjct: 672 WRPRFRYYHWALSF MGM-----SICLALMF I SSSWYYAIVAMVIAGM---- 712

Query: 715 SSWYYAIYKXIEYQSLSPHTDEDEWG DGI---XXXXXXXXXXXXEEGP---KNWRPQXXX 768
 IYK IEYQ E EWGDGI EEEGP KNWRPQ
 Sbjct: 713 ----IYKYIEYQGA---EKEWDGIRGLSLSAARFALLRLEEGPPHTKNWRPQLLV 761

Query: 769 XXXXXX-----XXXTFASQLKG NFLHVVKAGKGXTIVGSVIV-----GEALAAEQT I 814
 TFASQL KAGKG TIVGSVIV GEALAAEQT I
 Sbjct: 762 LLKLDEDLHVKHPRLLTFASQL-----KAGKGLTIVGSVIVGNFLHN YGEALAAEQT I 814

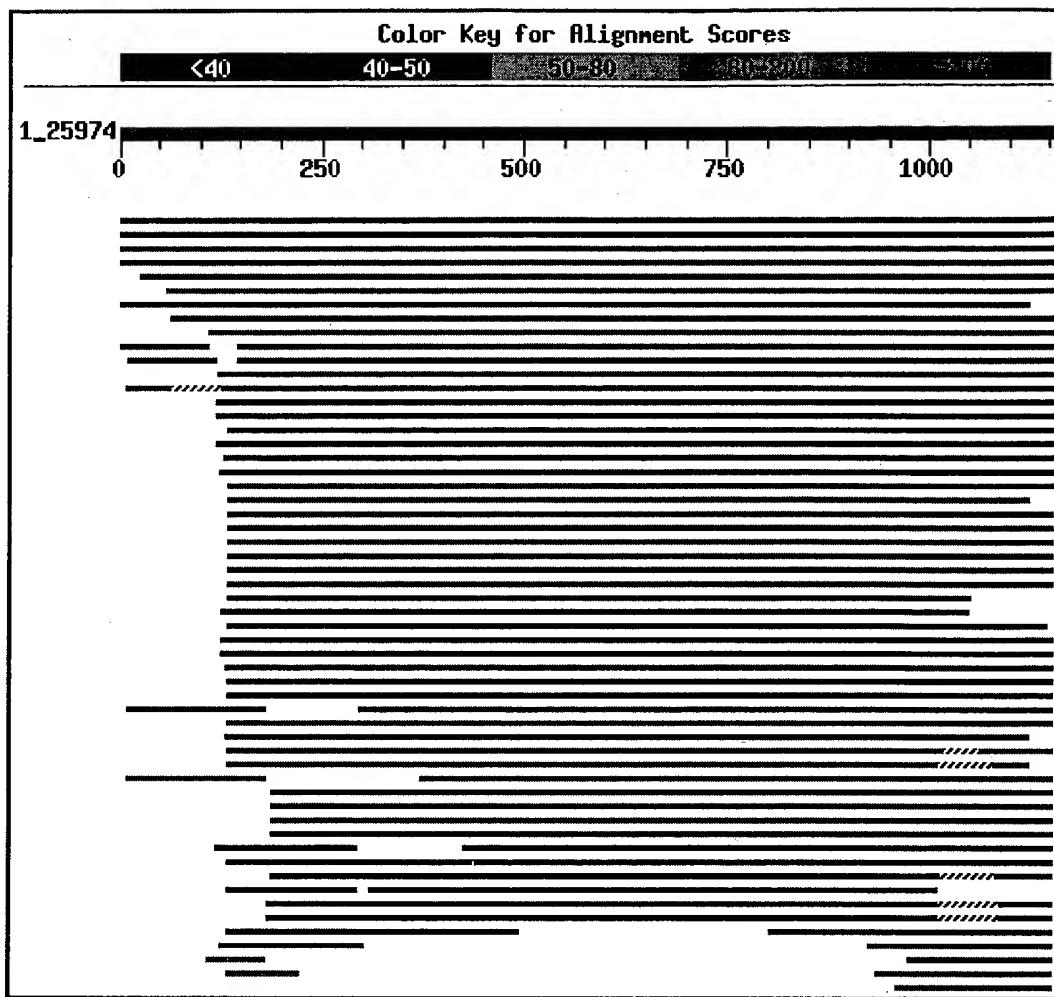
Query: 815 KHV VACGLLENYLMEA EKVKGFCQL---AKLREGISH-----GGMKHNTVVL IQSMGW 864
 KH LMEA EKVKGFCQL AKLREGISH GGMKHNTVV MGW
 Sbjct: 815 KH-----LMEA EKVKGFCQLVVA AKLREGISH LIQSCGLGGMKHN TVV---MGW 860

Query: 865 PNGWRQSERVTTDARAWKTFIGTVKNINIDLPFAAH LALLVA---SFFPSNVEQFSEG-- 919
 PNGWRQSE DARAWKTFIGTV + AAHLALLVA SFFPSNVEQFSEG
 Sbjct: 861 PNGWRQSE---DARAWKTFIGTVR-----VTTAAH LALLVAKNISFFPSNVEQFSEGNI 911

Query: 920 -VWWIVHDGGMLML---LLKQHKVWRK-----TVAQLEDNSISCSIQMKATFLYHLRI E 969
 VWWIVHDGGMLML LLKQHKVWRK TVAQLEDNSI + ATFLYHLRI E
 Sbjct: 912 DVWWIVHDGGMLMLPFLLKQHKVWRKCSIRIFTVAQLEDNSIQMKKDL-ATFLYHLRI E 970

Query: 970 AEVRIFKDLEVVRTLEMHDSDISAYTYERHMRLSKMMEQRSQL-----TERDRIAQL 1022
 AEV + +EMHDSDISAYTYER + MMEQRSQL TERDR AQL
 Sbjct: 971 AEVEV-----VEMHDSDISAYTYERTL---MMEQRSQLRHMR LSKTERDREAQL 1017

Query: 1023 VKDRNSMLRLTSIGSXXXXXXXXXXXXYMAQDLLHTAVYQE KVHM-----SRGQ 1073
 VKDRNSMLRLTSIGS T YQE KVHM SRGQ
 Sbjct: 1018 VKDRNSMLRLTSIGSDEDE-----ETETYQE KVHM TWDKYM ASRGQ 1060



Score (bits)	E Value	
2531	0.0	G
2531	0.0	G
2499	0.0	G
2466	0.0	G
2444	0.0	G
2350	0.0	G
2345	0.0	
2294	0.0	G
2246	0.0	G
2221	0.0	G
2221	0.0	G
2212	0.0	G
1646	0.0	
1620	0.0	G
1614	0.0	G
1611	0.0	G

gi 45219767 gb AAH66872.1	Solute carrier family 12, member...	1611	0.0	
gi 27151684 sp Q28677 S124	RABIT Solute carrier family 12 m...	1608	0.0	
gi 31324218 gb AAP47188.1	potassium-chloride cotransporter...	1607	0.0	
gi 4827006 ref NP_005063.1	solute carrier family 12 (potas...	1602	0.0	
gi 3015641 gb AAC39685.1	erythroid K:Cl cotransporter spli...	1511	0.0	
gi 19705463 ref NP_599190.1	solute carrier family 12 membe...	1431	0.0	
gi 11968148 ref NP_065759.1	solute carrier family 12 membe...	1426	0.0	
gi 14193696 gb AAK56093.1	K-Cl cotransporter [Mus musculus]	1426	0.0	
gi 33859680 ref NP_065066.1	solute carrier family 12, memb...	1426	0.0	
gi 12003227 gb AAG43493.1	electroneutral potassium-chlorid...	1426	0.0	
gi 28972652 dbj BAC65742.1	mKIAA1176 protein [Mus musculus]	1426	0.0	
gi 3015639 gb AAC39684.1	erythroid K:Cl cotransporter spli...	1415	0.0	
gi 50753670 ref XP_414082.1	PREDICTED: similar to K-Cl cot...	1413	0.0	
gi 6330233 dbj BAA86490.1	KIAA1176 protein [Homo sapiens]	1398	0.0	
gi 5730043 ref NP_006589.1	solute carrier family 12 (potas...	1378	0.0	
gi 47225214 emb CAF98841.1	unnamed protein product [Tetrao...	1374	0.0	
gi 50733496 ref XP_418891.1	PREDICTED: similar to mFLJ0009...	1373	0.0	
gi 6755534 ref NP_035520.1	solute carrier family 12, membe...	1365	0.0	
gi 47847414 dbj BAD21379.1	mFLJ00098 protein [Mus musculus]	1365	0.0	
gi 9651224 gb AAF91094.1	K-Cl cotransporter KCC1 [Mus musc...	1339	0.0	
gi 32490535 gb AAP84988.1	potassium-chloride cotransporter...	1318	0.0	
gi 47213000 emb CAF95392.1	unnamed protein product [Tetrao...	1147	0.0	
gi 47220725 emb CAG11794.1	unnamed protein product [Tetrao...	1136	0.0	
gi 47223173 emb CAG11308.1	unnamed protein product [Tetrao...	1113	0.0	
gi 10440500 dbj BAB15783.1	FLJ00098 protein [Homo sapiens]	999	0.0	
gi 21429886 gb AAM50621.1	GH09271p [Drosophila melanogaste...	985	0.0	
gi 24762439 ref NP_726378.1	CG5594-PA [Drosophila melanoga...	985	0.0	
gi 46409210 gb AAS93762.1	LD02554p [Drosophila melanogaste...	974	0.0	
gi 22026947 ref NP_571976.2	CG5594-PC [Drosophila melanoga...	974	0.0	
gi 10440514 dbj BAB15787.1	FLJ00105 protein [Homo sapiens]	954	0.0	
gi 34853395 ref XP_217744.2	similar to putative potassium-...	893	0.0	
gi 48096020 ref XP_394587.1	similar to CG5594-PC [Apis mel...	843	0.0	
gi 31226974 ref XP_317803.1	ENSANGP00000014479 [Anopheles ...	644	0.0	
gi 25149428 ref NP_500910.2	solute carrier family 12 membe...	584	e-165	
gi 39584234 emb CAE61609.1	Hypothetical protein CBG05529 [...	578	e-163	
gi 13507237 gb AAK28520.1	K-Cl cotransporter [Xenopus laevis]	552	e-155	
gi 26343083 dbj BAC35198.1	unnamed protein product [Mus mu...	490	e-136	
gi 32484273 gb AAH54325.1	LOC398663 protein [Xenopus laevis]	474	e-132	
gi 15208177 dbj BAB63113.1	hypothetical protein [Macaca fa...	439	e-121	
gi 31226957 ref XP_317800.1	ENSANGP00000004794 [Anopheles ...	421	e-115	
gi 47203569 emb CAG13773.1	unnamed protein product [Tetrao...	389	e-106	
gi 9651629 gb AAF91220.1	potassium-chloride cotransporter ...	375	e-102	
gi 18073139 emb CAC80545.1	putative Na-K-Cl cotransporter ...	365	5e-99	
gi 38073246 gb AAR10807.1	K-Cl cotransporter KCC3a isoform...	356	4e-96	
gi 17541928 ref NP_501141.1	solute carrier family 12 membe...	329	5e-88	
gi 35505532 gb AAH57624.1	Slc12a5 protein [Mus musculus]	326	4e-87	
gi 38073248 gb AAR10808.1	brain-specific K-Cl cotransport...	324	2e-86	
gi 39596034 emb CAE67537.1	Hypothetical protein CBG13060 [...	296	3e-78	
gi 9651216 gb AAF91090.1	K-Cl cotransporter [Mus musculus]	284	2e-74	

<u>gi 47193414 emb CAG14039.1 </u>	unnamed protein product [Tetrao...	<u>283</u>	<u>4e-74</u>	
<u>gi 7512576 pir T17231</u>	hypothetical protein DKFZp434F076.1 ...	<u>279</u>	<u>4e-73</u>	G
<u>gi 3925714 emb CAA09464.1 </u>	KCC2 protein [Mus musculus]	<u>267</u>	<u>2e-69</u>	G
<u>gi 3582769 gb AAC35282.1 </u>	erythrocyte K-Cl cotransporter [H...	<u>262</u>	<u>6e-68</u>	G
<u>gi 31226979 ref XP_317804.1 </u>	ENSANGP00000024771 [Anopheles ...	<u>261</u>	<u>2e-67</u>	G
<u>gi 14043556 gb AAH07760.1 </u>	SLC12A7 protein [Homo sapiens]	<u>252</u>	<u>6e-65</u>	G
<u>gi 17534831 ref NP_495555.1 </u>	Na-K-Cl cotransporter (2H716) ...	<u>236</u>	<u>3e-60</u>	G
<u>gi 31226967 ref XP_317802.1 </u>	ENSANGP00000015001 [Anopheles ...	<u>230</u>	<u>3e-58</u>	G
<u>gi 34857570 ref XP_345417.1 </u>	similar to K-Cl cotransporter ...	<u>229</u>	<u>5e-58</u>	G
<u>gi 37575103 gb AAQ93478.1 </u>	furosemide-sensitive KCl cotrans...	<u>221</u>	<u>2e-55</u>	
<u>gi 1673531 gb AAB18960.1 </u>	furosemide-sensitive K-Cl cotrans...	<u>217</u>	<u>2e-54</u>	
<u>gi 39593544 emb CAE61836.1 </u>	Hypothetical protein CBG05808 [...]	<u>216</u>	<u>3e-54</u>	
<u>gi 50778569 ref XP_427392.1 </u>	PREDICTED: similar to solute c...	<u>191</u>	<u>2e-46</u>	G
<u>gi 38073244 gb AAR10806.1 </u>	K-Cl cotransporter KCC3b isoform...	<u>167</u>	<u>3e-39</u>	
<u>gi 30691724 ref NP_849732.1 </u>	cation-chloride cotransporter,...	<u>138</u>	<u>1e-30</u>	G
<u>gi 34905658 ref NP_914176.1 </u>	putative cation-chloride co-tr...	<u>134</u>	<u>3e-29</u>	G
<u>gi 50944163 ref XP_481609.1 </u>	putative Na ⁺ /K ⁺ /Cl ⁻ -cotransport...	<u>133</u>	<u>5e-29</u>	
<u>gi 52075682 dbj BAD44902.1 </u>	putative potassium-chloride cot...	<u>132</u>	<u>9e-29</u>	
<u>gi 16417791 gb AAL18853.1 </u>	potassium chloride cotransporter...	<u>131</u>	<u>2e-28</u>	
<u>gi 2582381 gb AAC49874.1 </u>	cation-chloride co-transporter [N...	<u>123</u>	<u>4e-26</u>	
<u>gi 20151457 gb AAM11088.1 </u>	GH27027p [Drosophila melanogaste...	<u>118</u>	<u>1e-24</u>	G
<u>gi 31242251 ref XP_321556.1 </u>	ENSANGP00000011560 [Anopheles ...	<u>118</u>	<u>2e-24</u>	G
<u>gi 516001 gb AAC48592.1 </u>	bumetanide-sensitive Na-K-Cl cotra...	<u>112</u>	<u>1e-22</u>	
<u>gi 1079521 gb AAC52633.1 </u>	kidney-specific Na-K-Cl cotranspo...	<u>112</u>	<u>1e-22</u>	G
<u>gi 2290526 gb AAB65150.1 </u>	Na-(K)-Cl cotransporter isoform m...	<u>112</u>	<u>1e-22</u>	G
<u>gi 21686589 gb AAM74968.1 </u>	renal Na-K-Cl cotransporter isof...	<u>111</u>	<u>2e-22</u>	
<u>gi 21686587 gb AAM74967.1 </u>	renal Na-K-Cl cotransporter isof...	<u>111</u>	<u>2e-22</u>	
<u>gi 25304083 gb AAH40138.1 </u>	Unknown (protein for MGC:48843) ...	<u>109</u>	<u>7e-22</u>	
<u>gi 6755532 ref NP_035519.1 </u>	solute carrier family 12, membe...	<u>109</u>	<u>7e-22</u>	G
<u>gi 34365781 ref NP_899197.1 </u>	solute carrier family 12, memb...	<u>109</u>	<u>7e-22</u>	G
<u>gi 16877251 gb AAH16888.1 </u>	Solute carrier family 12, member...	<u>109</u>	<u>7e-22</u>	G
<u>gi 27151793 sp P55014 S121_MOUSE</u>	Solute carrier family 12 m...	<u>109</u>	<u>7e-22</u>	G
<u>gi 40950187 gb AAR97733.1 </u>	Na-K-Cl cotransporter [Oreochrom...	<u>109</u>	<u>7e-22</u>	
<u>gi 9507103 ref NP_062007.1 </u>	solute carrier family 12, membe...	<u>108</u>	<u>2e-21</u>	G
<u>gi 38073242 gb AAR10805.1 </u>	K-Cl cotransporter KCC4 [Rattus ...	<u>107</u>	<u>4e-21</u>	G

Alignments

[Get selected sequences](#) [Select all](#) [Deselect all](#)

>gi|22416427|gb|AAM96215.1| **G** potassium-chloride transporter-3a [Homo sapiens]
gi|5106523|gb|AAD39742.1| **G** K-Cl cotransporter KCC3a [Homo sapiens]
gi|27151690|sp|Q9UHW9|S126_HUMAN **G** Solute carrier family 12 member 6 (Electroneut
 cotransporter 3) (K-Cl cotransporter 3)
 Length = 1150

Score = 2531 bits (5961), Expect = 0.0
 Identities = 926/1362 (67%), Positives = 930/1362 (68%), Gaps = 419/1362 (30%)

Query: 1 MHPETTTKMASVRFMVPTKIDDIPLGLSDTSPDXSSRSSSRVRFSSRESPETSRSEPM 60
 MHPETTTKMASVRFMVPTKIDDIPLGLSDTSPD SSRSSSRVRFSSRESPETSRSEPM
 Sbjct: 1 MHPETTTKMASVRFMVPTKIDDIPLGLSDTSPDLSSRSSSRVRFSSRESPETSRSEPM 60

Query: 61 SEMSDPPSDLSQNSGHKKAEGDEYMDTRPGATTSLATVAL----RTSHPQDVIED--- 111
 SEMS GATTSLATVAL RTSHPQDVIED
 Sbjct: 61 SEMS-----GATTSLATVALDPPSDRTSHPQDVIEDLSQN 95

Query: 112 -ITGEHSQQLDD---QRNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRM 155
 ITGEHSQQLDD RNAYLNNSNYE E +E FDKNLA KVSSLLNRM
 Sbjct: 96 SITGEHSQQLDDGHKKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRM 153

Query: 156 ANY---QGAKEHEEAENITNLTEGKKKPTKTPQMG-----LQNIFGVTFMGVYI 202
 ANY QGAKEHEEAENIT EGKKKPTKTPQMG LQNIFGV I
 Sbjct: 154 ANYTNLTQGAKEHEEAENIT---EGKKKPTKTPQMGTFMGVYLPCLQNIIFGV----I 203

Query: 203 LFLRLLPCTWVVGTAGVLQAFIAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 262
 LFLRL TWVVGTAGVLQAFIAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL
 Sbjct: 204 LFLRL---TWVVGTAGVLQAFIAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 260

Query: 263 GPYLGTTFEIFLVYEFGGAVGLCF----AAAMYILGAI----IVPRAAIFHSDDAL 310
 GP EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDAL
 Sbjct: 261 GP-----EFGGAVGLCFYLGTTFAAAMYILGAIIEIFLVYIVPRAAIFHSDDAL 308

Query: 311 KESAAMLNMRVYGTAFLVLMLVVFFIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFA 370
 KESAAMLNMRVYGTAFLVLMLVVFFIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFA
 Sbjct: 309 KESAAMLNMRVYGTAFLVLMLVVFFIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFA 368

Query: 371 PPHFPVCMLGNRTLSS--IDVCSKTKEINNMTRHVPSK-----NATCDECNSS 416
 PPHFPVCMLGNRTLSS IDVCSKTKEINNMTRHVPSK NATCDEC
 Sbjct: 369 PPHFPVCMLGNRTLSSRHDVCSKTKEINNMTRHVPSK-----VPSKLWGFFCNSSQFFNATCDE--- 422

Query: 417 YFVHNNVQFFTSIQGIPGLASGIITENLWSNYLPKGEIEK---SSDVLGSLNHEYVVLV 472
 YFVHNNV TSIQGIPGLASGIITENLWSNYLPKGEIEK SSDVLGSLNHEYVVLV
 Sbjct: 423 YFVHNNV---TSIQGIPGLASGIITENLWSNYLPKGEIEKPSAKSSDVLGSLNHEYVVLV 479

Query: 473 DPSAKITTSFTLLVGIFFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTSLWGFFFV 532
 D ITTSFTLLVGIFFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS FV
 Sbjct: 480 D---ITTSFTLLVGIFFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS---FV 530

Query: 533 YLSNVVLFGACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIVI 584
 YLSNVVLFGACIEGVVLRDKFG DAVKGNLV PWVIVI
 Sbjct: 531 YLSNVVLFGACIEGVVLRDKFG-----DAVKGNLVVGTLSPSPWVIVI 574

Query: 585 GS-----LQSLDNITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT-- 626
 GS LQSL TGAP RLLQAIK VFGHSKANGEPT
 Sbjct: 575 GSFFSTCGAGLQSL---TGAP-----RLLQAIKDNIIPFLRVFGHSKANGEPTWA 622

Query: 627 -----GILIASLDFFLMCYLTLLRLTAALVAPIELILSM-----CA 664
 GILIASLD LVAPI LSM CA
 Sbjct: 623 LLLTAAIAELGILIASLD-----LVAPI---LSMFFLMCYLFVNLA CA 662

Query: 665 LQ-----RYYHWALSFMGTPNWVNLRPRPRFSICLALMF-----VAMV 705
 LQ RYYHWALSFMG SICLALMF VAMV
 Sbjct: 663 LQTLLRTPNWRPRFRYYHWALSFMG-----SICLALMFISSWYYAIVAMV 708

Query: 706 IAGMIGAEKSSWYYAIYKXIEYQSLSPHTDEDEWDGIRGL---AARFALLRLEEGP--- 759
 IAGM IYK IEYQ E EWGDGIRGL AARFALLRLEEGP
 Sbjct: 709 IAGM-----IYKYIEYQG-----AEKEWGDGIRGLSLSAARFALLRLEEGPPHT 752

Query: 760 KNWRPQLLVLLKL-----HPRLLTFASQLKGNFLHVKAGKGXTIVGSVIVG----- 805
 KNWRPQLLVLLKL HPRLLTFASQLK AGKG TIVGSVIVG
 Sbjct: 753 KNWRPQLLVLLKLDDELHVKHPRLLTFASQLK-----AGKGLTIVGSVIVGNFLENYG 805

Query: 806 EALAAEQTIKHVVACGLLENYLMEAEEKVKGFCQL---AKLREGISH-----GGMKHNT 855
 EALAAEQTIKH LMEAEEKVKGFCQL AKLREGISH GGMKHNT
 Sbjct: 806 EALAAEQTIKH-----LMEAEEKVKGFCQLVVAKILREGISHLIQSCGLGGMKHNT 855

Query: 856 VVLIQSMGWPNWRQSERVTTDARAWKTFIGTVKNINIDLPFAAHLLVA---SFFPSN 912
 VV MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSN
 Sbjct: 856 VV---MGWPNGWRQSE---DARAWKTFIGTVR-VTT---AAHLALLVAKNISFFPSN 902

Query: 913 VEQFSEG---VWWIVHDGGMLMLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK- 959
 VEQFSEG VWWIVHDGGMLMLL LKQHKVWRK TVAQLEDNSI QMK
 Sbjct: 903 VEQFSEGNIDVWWIVHDGGMLMLLPFLLKQHKVWRKCSIRIFTVAQLEDNSI---QMKK 958

Query: 960 --ATFLYHLRIEAEVRIFKDLEVVRTLEMHDSDISAYTYERHMRLSKMMEQRSQML--- 1013
 ATFLYHLRIEAEV EVV EMHDSDISAYTYER + MMEQRSQML
 Sbjct: 959 DLATFLYHLRIEAEV-----EVV---EMHDSDISAYTYERTL---MMEQRSQMLRHMR 1005

Query: 1014 ---TERDRIAQLVKDRNSMLRLTSIGSDEDEETETTWTKDQYMAQDLLHTAVYQEKVHM- 1069
 TERDR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM
 Sbjct: 1006 LSKTERDREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHMT 1048

Query: 1070 -----SRGQKAKSMEGF---NMRPDQSNVRRM---KLNEVIVNKSHEAKLVLLNM 1113
 SRGQKAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNM
 Sbjct: 1049 WTKDKYMASRGQKAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNM 1108

Query: 1114 PGPPRNPEGDENYMEFLEVTEGLERVLLVRGGGSEVITIYS 1155
 PGPPRNPEGDENYMEFLEVTEGLERVLLVRGGGSEVITIYS
 Sbjct: 1109 PGPPRNPEGDENYMEFLEVTEGLERVLLVRGGGSEVITIYS 1150

>gi|6693798|gb|AAF24986.1|  K-Cl cotransporter KCC3 [Homo sapiens]
 Length = 1150

Score = 2531 bits (5961), Expect = 0.0
 Identities = 926/1362 (67%), Positives = 930/1362 (68%), Gaps = 419/1362 (30%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDXSSRSSRVRFSSRESPVPETSRSEPM 60
 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPD SSRRSSRVRFSSRESPVPETSRSEPM
 Sbjct: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDLSSRSSRVRFSSRESPVPETSRSEPM 60

Query: 61 SEMSDPPSDLSQNSGHKKAEGDEYMDTRPGATTSLATVAL-----RTSHPQDVIED--- 111
 SEMS GATTSLATVAL RTSHPQDVIED
 Sbjct: 61 SEMS-----GATTSLATVALDPPSDRTSHPQDVIEDLSQN 95

Query: 112 -ITGEHSQLDD---QRNAYLNNNSNYELFE-EESFDKNLA-----KVSSLLNRM 155
 ITGEHSQLDD RNAYLNNNSYE E +E FDKNLA KVSSLLNRM
 Sbjct: 96 SITGEHSQLDDGKKARNAYLNNNSYE--EGDEYFDKNALFEEEMDTRPKVSSLLNRM 153

Query: 156 ANY----QGAKEHEEAENITNLTEGKKPTKTPQMG-----LQNIFGVTFMGVYI 202
 ANY QGAKEHEEAENIT EGKKKPTKTPQMG LQNIFGV I
 Sbjct: 154 ANYTNLTQGAKEHEEAENIT---EGKKKPTKTPQMGTFMGVYLPCLQNIQGV-----I 203

Query: 203 LFLRLLPCTWVVGTAGVLQAFALICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 262
 LFLRL TWVVGTAGVLQAFALICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL
 Sbjct: 204 LFLRL---TWVVGTAGVLQAFALICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 260

Query: 263 GPYLGTTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDAL 310
 GP EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDAL
 Sbjct: 261 GP-----EFGGAVGLCFYLGTTFAAAMYILGAIIEIFLVYIVPRAAIFHSDDAL 308

Query: 311 KESAAMLNMRVYGTAFVLMLVVFFIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFA 370
 KESAAMLNMRVYGTAFVLMLVVFFIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFA
 Sbjct: 309 KESAAMLNMRVYGTAFVLMLVVFFIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFA 368

Query: 371 PPHFPVCMLGNRTLSS--IDVCSKTKEINNMTRHVP SK-----NATCDECNSS 416
 PPHFPVCMLGNRTLSS IDVCSKTKEINNM VPSK NATCDE
 Sbjct: 369 PPHFPVCMLGNRTLSSRHDVCSKTKEINNM--VPSKLWGFFCNSSQFFNATCDE--- 422

Query: 417 YFVHNNVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIIEK---SSDVLGSLNHEYVLV 472
 YFVHNNV TSIQGIPGLASGIITENLWSNYLPKGEIIIEK SSDVLGSLNHEYVLV
 Sbjct: 423 YFVHNNV---TSIQGIPGLASGIITENLWSNYLPKGEIIIEKPSAKSSDVLGSLNHEYVLV 479

Query: 473 DPSAKITTSFTLLVGIFFPSVTGIMAGSNRGDLKDAQKSIPIGТИLAILTTSIWGFFFV 532
 D ITTSFTLLVGIFFPSVTGIMAGSNRGDLKDAQKSIPIGТИLAILTTS FV
 Sbjct: 480 D---ITTSFTLLVGIFFPSVTGIMAGSNRGDLKDAQKSIPIGТИLAILTTS---FV 530

Query: 533 YLSNVVLFGACIEGVVLRDKFGVGTL SWPSFFSTCGAGDAVKGNLV-----PWVIVI 584
 YLSNVVLFGACIEGVVLRDKFG DAVKGNLV PWVIVI
 Sbjct: 531 YLSNVVLFGACIEGVVLRDKFG-----DAVKGNLVVGTL SWPSPWVIVI 574

Query: 585 GS-----LQSLDNIITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT-- 626
 GS LQSL TGAP RLLQAIK VFGHSKANGEPT
 Sbjct: 575 GSFFSTCGAGLQSL---TGAP-----RLLQAIKDNIIPFLRVFGHSKANGEPTWA 622

Query: 627 -----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----CA 664
 GILIASLD LVAPI LSM CA
 Sbjct: 623 LLLTAAIAELGILIASLD-----LVAPI---LSMFFLMCYLFVN LACA 662

Query: 665 LQ-----RYYHWALSFMGMTPNWVNLRPRPRFSICLALMFI-----VAMV 705
 LQ RYYHWALSFMG SICLALMFI VAMV
 Sbjct: 663 LQTLLRTPNWRPRFRYYHWALSFMG-----SICLALMFISWYYAIVAMV 708

Query: 706 IAGMIGAEKSSWYYAIYKXIEYQSLSPHTDEDEWDGIRGL---AARFALLRLEEGP--- 759
 IAGM IYK IEYQ E EWGDGIRGL AARFALLRLEEGP
 Sbjct: 709 IAGM-----IYKYIEYQG---AEKEWDGIRGLSLSAARFALLRLEEGPPHT 752

Query: 760 KNWRPQLLVLLKL-----HPRLLTFA SQLKGNFLHV KAGKGXTIVGSVIVG----- 805
 KNWRPQLLVLLKL HPRLLTFA SQLK AGKG TIVGSVIVG
 Sbjct: 753 KNWRPQLLVLLKLDEDLHV KHPRLLTFA SQLK-----AGKGLTIVGSVIVGNFLHNYG 805

Query: 806 EALAAEQTIKHVVACGLLENYLMEA KVKGFCQL---AKLREGISH-----GGMKHNT 855
 EALAAEQTIKH LMEA KVKGFCQL AKLREGISH GGMKHNT
 Sbjct: 806 EALAAEQTIKH-----LMEA KVKGFCQLVVA KLREGISH LIQSCGLGGMKHNT 855

Query: 856 VVLIQSMGWPNWRQSERVTTDARAWKTFIGTVKNIIDLPFAAHLLVA---SFFPSN 912
 VV MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSN
 Sbjct: 856 VV---MGWPNGWRQSE---DARAWKTFIGTVR-VTT---AAHLALLVAKNISFFPSN 902

Query: 913 VEQFSEG---VWWIVHDGGMLMLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK- 959
 VEQFSEG VWWIVHDGGMLMLL LKQHKVWRK TVAQLEDNSI QMK
 Sbjct: 903 VEQFSEGNIDVWWIVHDGGMLMLPFLLKQHKVWRKCSIRIFTVAQLEDNSI---QMKK 958

Query: 960 --ATFLYHLRIAEVRIFKDLEVVRTLEMHDSDISAYTYERHMRLSKMMEQRSQML--- 1013
 ATFLYHLRIAEV EVV EMHDSDISAYTYER + MMEQRSQML
 Sbjct: 959 DLATFLYHLRIAEV-----EVV---EMHDSDISAYTYERTL---MMEQRSQMLRHMR 1005

Query: 1014 ---TERDRIAQLVKDRNSMLRLTSIGSDEDEETETWTKDKYMAQDLLHTAVYQEKVHM- 1069
TERDR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM
Sbjct: 1006 LSKTERDREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHMT 1048

Query: 1070 -----SRGQKAKSMEGF---NMRPDQSNVRRM---KLNEVIVNKSHEAKLVLLNM 1113
SRGQKAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNM
Sbjct: 1049 WTKDKYMASRGQKAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNM 1108

Query: 1114 PGPPRNPEGDENYMEFLEVTEGLERVLLVRGGGSEVITIYS 1155
PGPPRNPEGDENYMEFLEVTEGLERVLLVRGGGSEVITIYS
Sbjct: 1109 PGPPRNPEGDENYMEFLEVTEGLERVLLVRGGGSEVITIYS 1150

>gi|33329252|gb|AAQ10026.1| **G** K-Cl cotransporter KCC3a-X2M isoform [Homo sapiens
Length = 1135

Score = 2499 bits (5886), Expect = 0.0
Identities = 916/1356 (67%), Positives = 920/1356 (67%), Gaps = 422/1356 (31%)

Query: 1 MHPETTTKMASVRFMVTPTKIDDIPLGLSDTSPDXSSRSSSRVRFSSRESPSRSEPM 60
MHPETTTKMASVRFMVTPTKIDDIPLGLSDTSPD SSRSSSRVRFSSRESPSRSEPM 60
Sbjct: 1 MHPETTTKMASVRFMVTPTKIDDIPLGLSDTSPDLSSRSSRVRFSSRESPSRSEPM 60

Query: 61 SEMSDPPSDLSQNSGHKKAEGDEYMDTRPGATTSLATVAL-----RTSHPQDVIEDITGE 115
SEMS GATTSLATVAL RTSHPQDVIED
Sbjct: 61 SEMS-----GATTSLATVALDPPSDRTSHPQDVIED--- 91

Query: 116 HSQLLDDQ---RNAYLNNNSNYELFE-EESFDKNLA-----KVSSLLNRMANY--- 158
D RNAYLNNNSYE E +E FDKNLA KVSSLLNRMANY
Sbjct: 92 -----DGHKKARNAYLNNNSYE--EGDEYFDKNALFEEEMDTRPKVSSLLNRMANYTNL 144

Query: 159 -QGAKEHEEAENITNLTEGKKKPTKTPQMG-----LQNIFGVTFMGVYILFLRL 208
QGAKEHEEAENIT EGKKKPTKTPQMG LQNIFGV ILFLRL
Sbjct: 145 TQGAKEHEEAENIT---EGKKKPTKTPQMGTFMGVYLPCLQNIFGV-----ILFLRL- 193

Query: 209 PCTWVVTAGVLQAFIAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLGT 268
TWVVTAGVLQAFIAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP
Sbjct: 194 --TWVVTAGVLQAFIAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP--- 247

Query: 269 TFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIHSDDALKESAAM 316
EFGGAVGLCF AAAMYILGAI IVPRAAIHSDDALKESAAM
Sbjct: 248 -----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIHSDDALKESAAM 299

Query: 317 LNNMRVYGTAFLVLMLVVFFIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFAPPHPV 376
LNNMRVYGTAFLVLMLVVFFIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFAPPHPV
Sbjct: 300 LNNMRVYGTAFLVLMLVVFFIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFAPPHPV 359

Query: 377 CMLGNRTLSS-IDVCSKTKEINNMTRHVP SK-----NATCDECNSSYFVHN 422
CMLGNRTLSS IDVCSKTKEINNM VPSK NATCDE YFVHN
Sbjct: 360 CMLGNRTLSSRHDVCSKTKEINNM VPSK LWGFFCNSSQFFNATCDE---YFVHN 413

Query: 423 VQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK---SSDVLGSLNHEYVLVDPSAKI 478
V TSIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLGSLNHEYVLVD I
Sbjct: 414 V---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLVD---I 466

Query: 479 TTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTSLWGFFFVYLSNV 538
TTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS FVYLSNV
Sbjct: 467 TTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS---FVYLSNV 521

Query: 539 LFGACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIVIGS---- 586
 LFGACIEGVVLRDKFG DAVKGNLV PWVIVIGS
 Sbjct: 522 LFGACIEGVVLRDKFG-----DAVKGNLVVGTLSWPSPWVIVIGSFFST 565

Query: 587 ----LQSLDNIITGAPPFLRWALLRLQAIAK-----VFGHSKANGEPT----- 626
 LQSL TGAP RLLQAIAK VFGHSKANGEPT
 Sbjct: 566 CGAGLQSL---TGAP-----RLLQAIAKDNIIPFLRVFGHSKANGEPTWALLTAA 613

Query: 627 ----GILIASLDFFLMCYLFLLRLTAALVAPIAELILSM-----CALQ---- 666
 GILIASLD LVAPI LSM CALQ
 Sbjct: 614 IAEGLGILIASLD-----LVAPI---LSMFFLMLCYLFVNLAACALQTLLR 653

Query: 667 -----RYYHWALSFMGMTPNWVNLRPRPRFSICLALMF-----VAMVIAGMIG 711
 RYYHWALSFMGML SICLALMF VAMVIAGM
 Sbjct: 654 TPNWRPRFRYYHWALSFMGML-----SICLALMFISSWYYAIVAMVIAGM-- 697

Query: 712 AEKSSWYYAIYKXIEYQSLSPHTDEDEWDGDIRGL--AARFALLRLEEGP---KNWRPQ 765
 TYK IEYQ E EWGDGIRGL AARFALLRLEEGP KNWRPQ
 Sbjct: 698 -----IYKYIEYQG-----AEKEWDGIRGLSAAARFALLRLEEGPPHTKNWRPQ 743

Query: 766 LLVLLKL-----HPRLLTFAQLGNFLHVAKGKXTIVGSIVG-----EALAAE 811
 LLVLLKL HPRLLTFAQLK AGKG TIVGSIVG EALAAE
 Sbjct: 744 LLVLLKLDEDLHVKHPRLLTFAQLK-----AGKGLTIVGSIVGNFLENYGEALAAE 796

Query: 812 QTIKHHVACGLLENYLMEAEKVKGFCQL--AKLREGISH-----GGMKHNTVVLIQS 861
 QTIKH LMEAEKVKGFCQL AKLREGISH GGMKHNTVV
 Sbjct: 797 QTIKH-----LMEAEKVKGFCQLVVAKLREGISHLIQSCGLGGMKHNTVV---- 842

Query: 862 MGWPNGWRQSERVTTDARAWKTFIGTVKNINIDLPFAAHLLVA--SFFPSNVEQFSE 918
 MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSNVEQFSE
 Sbjct: 843 MGWPNGWRQSE---DARAWKTFIGTVR-VTT---AAHLALLVAKNISFFPSNVEQFSE 893

Query: 919 G---VWWIVHDGGMLMLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK---ATFL 963
 G VWWIVHDGGMLMLL LKQHKVWRK TVAQLEDNSI QMK ATFL
 Sbjct: 894 GNIDVWWIVHDGGMLMLLPFLLKQHKVWRKCSIRIFTVAQLEDNSI---QMKKDLATFL 949

Query: 964 YHLRIEAEVRIFKDLEVVRTLEMHDSDISAYTYERHMRLSKMMEQRSQL-----TER 1016
 YHLRIEAEV EVV EMHDSDISAYTYER + MMEQRSQL TER
 Sbjct: 950 YHLRIEAEV-----EVV--EMHDSDISAYTYERTL---MMEQRSQLRHMRSLSKTER 996

Query: 1017 DRIAQLVKDRNSMLRLTSIGSDEDEETETTWTKDKYMAQDLLHTAVYQEKVHM----- 1069
 DR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM
 Sbjct: 997 DREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHMTWTKDKY 1039

Query: 1070 --SRGQKAKSMEGF---NMRPDQSNVRRM---KLNEVIVNKSHEAKLVLLNMPGPPRN 1119
 SRGQKAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNMPGPPRN
 Sbjct: 1040 MASRGQKAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNMPGPPRN 1099

Query: 1120 PEGDENYMEFLEVTEGLERVLLVRGGGSEVITIYS 1155
 PEGDENYMEFLEVTEGLERVLLVRGGGSEVITIYS
 Sbjct: 1100 PEGDENYMEFLEVTEGLERVLLVRGGGSEVITIYS 1135

>gi|41281645|ref|NP_598410.1| **G** solute carrier family 12, member 6 [Mus musculus]
 gi|15042077|gb|AAK81895.1| **G** K-Cl cotransporter 3a [Mus musculus]
 gi|27151686|sp|Q924N4|S126_MOUSE Solute carrier family 12 member 6 (Electroneutral
 cotransporter 3) (K-Cl cotransporter 3)
 Length = 1150

Score = 2466 bits (5808), Expect = 0.0
 Identities = 907/1362 (66%), Positives = 923/1362 (67%), Gaps = 419/1362 (30%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDXSSRSSSRVRFSSRESPVETSRSEPM 60
 MHPPE TTKM+SVRFMVTPTKIDDIPGLSDTSPD SSRSSSRVRFSSRESPVETSRSEPM
 Sbjct: 1 MHPPEATTKMSVRFMVTPTKIDDIPGLSDTSPDLSSRSSRVRFSSRESPVETSRSEPM 60

Query: 61 SEMSDPPSDLSQNSGHKKAEGDEYMDTRPGATTSLATVAL-----RTSHPQDVIED---- 111
 SE+S GATTSLATVAL RTS+PQDV ED
 Sbjct: 61 SELS-----GATTSLATVALDPSSDRTSNPQDVTEDPSQN 95

Query: 112 -ITGEHSQLLDD---QRNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRM 155
 ITGEHSQLLDD RNAYLNNSNYE E +E FDKNLA KVSSLLNRM
 Sbjct: 96 SITGEHSQLLDDGHKKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRM 153

Query: 156 ANY---QGAKEHEEAENITNLTEGKKKPTKTPQMG-----LQNIFGVTFMGVYI 202
 ANY QGAKEHEEAENIT EGKKKPTK+PQMG LQNIFGV I
 Sbjct: 154 ANYTNLTQGAKEHEEAENIT---EGKKKPTKSPQMGTFMGVYLPCLQNIFGV-----I 203

Query: 203 LFLRLLPCTWVVGTAGVLQAFIAVLIICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 262
 LFLRL TWVVGTAG+LQAFIAVLIICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL
 Sbjct: 204 LFLRL---TWVVGTAGILQAFIAVLIICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 260

Query: 263 GPYLGTTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDAL 310
 GP EFGGAVGLCF AAAMYILGAI IVPRAAIF SDDAL
 Sbjct: 261 GP-----EFGGAVGLCFYLGTTFAAAMYILGATEIFLVYIVPRAAIFRSDDAL 308

Query: 311 KESAAMLNMRVYGTAFVLMLVLFVFIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFA 370
 KESAAMLNMRVYGTAFVLMLVLFVFIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFA
 Sbjct: 309 KESAAMLNMRVYGTAFVLMLVLFVFIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFA 368

Query: 371 PPHFPVCMLGNRTLSS--IDVCSKTKEINNMTRHVP SK-----NATCDECNSS 416
 PPHFPVCMLGNRTLSS +D+CSKTKE++NMT VPSK NATCDE
 Sbjct: 369 PPHFPVCMLGNRTLSSRHLDCSKTKEVDNMT--VPSKLWGFFCNSSQFFNATCDE---- 422

Query: 417 YFVHNNSQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK---SSDVLGSLNHEYVLV 472
 YFVHNNS SIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLG+LNHEYVL
 Sbjct: 423 YFVHNNS---ISIYGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGNLNHEYVLA 479

Query: 473 DPSAKITTSFTLLVGIFFPSVTGIMAGSNRGDLKDAQKSIPIGTILAILTSLWGFFFV 532
 D ITTSFTLLVGIFFPSVTGIMAGSNRGDLKDAQKSIPIGTILAILTTS FV
 Sbjct: 480 D---ITTSFTLLVGIFFPSVTGIMAGSNRGDLKDAQKSIPIGTILAILTTS----FV 530

Query: 533 YLSNVVLFGACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIVI 584
 YLSNVVLFGACIEGVVLRDKFG DAVKGNLV PWVIVI
 Sbjct: 531 YLSNVVLFGACIEGVVLRDKFG-----DAVKGNLVVGTLSWPSPWVIVI 574

Query: 585 GS-----LQSLDNIIITGAPPFLRWALLRLLQAIAK-----VFGHSKANGEPT-- 626
 GS LQSL TGAP RLLQAIAK VFGHSKANGEPT
 Sbjct: 575 GSFFSTCGAGLQSL---TGAP-----RLLQAIAKDNIIPFLRVFGHSKANGEPTWA 622

Query: 627 -----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----CA 664
 GILIASLD LVAPI LSM CA
 Sbjct: 623 LLLTAAIAELGILIASLD-----LVAPI---LSMFFLMCYLFVN LACA 662

Query: 665 LQ-----RYYHWALSFMGMTPNWVNLRPRPRFSICLALMFI-----VAMV 705
 LQ RYYHWALSFMG M SICLALMFI VAMV
 Sbjct: 663 LQTLLRTPNWRPRFRYYHWALSFMG-----SICLALMFISSSWYYAIVAMV 708

Query: 706 IAGMIGAEKSSWYYAIYKXIEYQSLSPHTDEDEWDGDIRGL---AARFALLRLEEGP--- 759
 IAGM IYK IEYQ E EWGDGIRGL AARFALLRLEEGP
 Sbjct: 709 IAGM-----IYKYIEYQG-----AEKEWDGDIRGLSLSAARFALLRLEEGPPHT 752

Query: 760 KNWRPQLLVLKL-----HPRLLTFASQLKGNFLHVKAGKGXTIVGSVIVG----- 805
 KNWRPQLLVLKL HPRLLTFASQLK AGKG TIVGSVIVG
 Sbjct: 753 KNWRPQLLVLKLDEDLHVKHPRLLTFASQLK-----AGKGLTIVGSVIVGNFLENYG 805

Query: 806 EALAAEQTICKHVVACGLLENYLMEAEKVKGFCQL---AKLREGISH-----GGMKHNT 855
 +ALAAEQTICKH LMEAEKVKGFCQL AKL+EGISH GGMKHNT
 Sbjct: 806 DALAAEQTICKH-----LMEAEKVKGFCQLVVAALKLEGISHLIQSCGLGGMKHNT 855

Query: 856 VVLIQSMGPNGWRQSERVTTDARAWKTFIGTVKNINIDLPFAAHLLVA---SFFPSN 912
 VV MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSN
 Sbjct: 856 VV---MGWPNGWRQSE---DARAWKTFIGTVR-VTT---AAHLALLVAKNVSFFPSN 902

Query: 913 VEQFSEG---VWWIVHDGGMLMLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK- 959
 VEQFSEG V WIVHDGGMLMLL LKQHKVWRK TVAQLEDNSI QMK
 Sbjct: 903 VEQFSEGNIDVRWIVHDGGMLLPFLLQHKVWRKCSIRIFTVAQLEDNSI---QMKK 958

Query: 960 --ATFLYHLRIEAEV RIFK DLEV VRTLEMHDSDISAYTYERHMRLSKMMEQRSQLM--- 1013
 ATFLYHLRIEAEV EVV EMHDSDISAYTYER + MMEQRSQLM
 Sbjct: 959 DLATFLYHLRIEAEV-----EVV---EMHDSDISAYTYERTL---MMEQRSQLMLRHMR 1005

Query: 1014 ---TERDRIAQLVKDRNSMLRLTSIGSDEDEETETTWTKDKYMAQDLLHTAVYQEKVHM- 1069
 TERDR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM
 Sbjct: 1006 LSKTERDREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHMT 1048

Query: 1070 -----SRGQKAKSMEGF---NMRPDQSNVRRM---KLNEVIVNKSHEAKLVLLNM 1113
 SRGQK KSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNM
 Sbjct: 1049 WTKDKYMASRGQKVKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNM 1108

Query: 1114 PGPPRNPEGDENYMEFLEVLT EGLERVLLVRGGGSEVITIYS 1155
 PGPPRNPEGDENYMEFLEVLT EGLERVLLVRGGGSEVITIYS
 Sbjct: 1109 PGPPRNPEGDENYMEFLEVLT EGLERVLLVRGGGSEVITIYS 1150

>gi|47124056|gb|AAH70107.1| **G** SLC12A6 protein [Homo sapiens]
 Length = 1156

Score = 2444 bits (5755), Expect = 0.0
 Identities = 900/1336 (67%), Positives = 904/1336 (67%), Gaps = 419/1336 (31%)

Query: 27 GLSDTSPDXSSRSSSRVRFSSRESPVPETSRSEPMSEMSDPPSDLSQNSGHKKAEGDEYMD 86
 GLSDTSPD SSRSSSRVRFSSRESPVPETSRSEPMSEMS
 Sbjct: 33 GLSDTSPDLSSRSSSRVRFSSRESPVPETSRSEPMSEMS----- 70

Query: 87 TRPGATTSLATVAL-----RTSHPQDVIED-----ITGEHSQLDD---QRNAYLNNSN 132
 GATTSLATVAL RTSHPQDVIED ITGEHSQLDD RNAYLNNSN
 Sbjct: 71 ---GATTSLATVALDPPSDRTSHPQDVIEDLSQNSITGEHSQLDDGHKKARNAYLNNSN 127

Query: 133 YELFE-EESFDKNLA-----KVSSLLNRMANY---QGAKEHEEAENITNLTT EG 177
 YE E +E FDKNLA KVSSLLNRMANY QGAKEHEEAENIT EG
 Sbjct: 128 YE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRMANYTNLTQGAKEHEEAENIT---EG 181

Query: 178 KKKPTKTPQMG-----LQN1FGVTFMGVYILFLRLLPCTWVVTAGVLQAFIAVLI 228
 KKKPTKTPQMG LQN1FGV ILFLRL TWVVGTAGVLQAFIAVLI
 Sbjct: 182 KKKPTKTPQMGTFMGVYPPCLQN1FGV-----ILFLRL---TWVVGTAGVLQAFIAVLI 232

Query: 229 CCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLGTTFEIFLVYEFGGAVGLCF-- 286
 CCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP EFGGAVGLCF
 Sbjct: 233 CCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP-----EFGGAVGLCFYL 280

Query: 287 ----AAAMYILGAI-----IVPRAAIFHSDDALKESAAMLNNMRVYGTAFLVLMVLVVF 336
 AAAMYILGAI IVPRAAIFHSDDALKESAAMLNNMRVYGTAFLVLMVLVVF
 Sbjct: 281 GTTFAAAAMYILGAIEIFLVYIVPRAAIFHSDDALKESAAMLNNMRVYGTAFLVLMVLVVF 340

Query: 337 IGVRYVNKFASXFLACVIVSILAIYAGAIKSSFAPPFPVCMLGNRTLSS--IDVCSKTK 394
 IGVRYVNKFAS FLACVIVSILAIYAGAIKSSFAPPFPVCMLGNRTLSS IDVCSKTK
 Sbjct: 341 IGVRYVNKFASLFLACVIVSILAIYAGAIKSSFAPPFPVCMLGNRTLSSRHIDVCSKTK 400

Query: 395 EINNMTRHPSK-----NATCDECNSSYFVHNNVQFFTSIQGIPGLASGIITE 442
 EINNMT VPSK NATCDE YFVHNNV TSIQGIPGLASGIITE
 Sbjct: 401 EINNMT--VPSKLWGFFCNSSQFFNATCDE---YFVHNNV---TSIQGIPGLASGIITE 451

Query: 443 NLWSNYLPKGEIIIEK---SSDVVLGSLNHEYVLVDPSAKITTSFTLLVGIFFFPSVTGIMA 498
 NLWSNYLPKGEIIIEK SSDVVLGSLNHEYVLVD ITTSFTLLVGIFFFPSVTGIMA
 Sbjct: 452 NLWSNYLPKGEIIIEKPSAKSSDVVLGSLNHEYVLVD---ITTSFTLLVGIFFFPSVTGIMA 507

Query: 499 GSNRSGDLKDAQKSIPIGTILAILTSLWGFVYLSNVVLFGACIEGVVLRDKFGVGTL 558
 GSNRSGDLKDAQKSIPIGTILAILTS FVYLSNVVLFGACIEGVVLRDKFG
 Sbjct: 508 GSNRSGDLKDAQKSIPIGTILAILTS---FVYLSNVVLFGACIEGVVLRDKFG--- 558

Query: 559 SWPSFFSTCGAGDAVKGNLV-----PWVIVIGS-----LQSLDNIITGAPPFLR 602
 DAVKGNLV PWVIVIGS LQSL TGAP
 Sbjct: 559 -----DAVKGNLVVGTLSWPSPWVIVIGSFFSTCGAGLQSL---TGAP--- 598

Query: 603 WALLRLLQAIAK-----VFGHSKANGEPT-----GILIASLDFFLMCYLF 642
 RLLQAIAK VFGHSKANGEPT GILIASLD
 Sbjct: 599 ---RLLQAIAKDNIIIPFLRVFGHSKANGEPTWALLTAAIAELGILIASLD----- 646

Query: 643 TLLRLTAALVAPIAELILSM-----CALQ-----RYYHWALSFMMG 678
 LVAPI LSM CALQ RYYHWALSFMMG
 Sbjct: 647 -----LVAPI---LSMFFLMLCYLFVNLAQCALQTLRTPNWRPRFRYYHWALSFMMG 694

Query: 679 TPNWVNLRPRPRFSICLALMF-----VAMVIAGMIGAEKSSWYYAIYKXIEYQSL 731
 SICLALMF VAMVIAGM IYK IEYQ
 Sbjct: 695 -----SICLALMFISSSWYYATVAMVIAGM-----IYKYIEYQG-- 727

Query: 732 PHTDEDEWGTDGIRGL---AARFALLRLEEGP---KNWRPQLLVLLKL-----HPRLLT 778
 E EWGDGIRGL AARFALLRLEEGP KNWRPQLLVLLKL HPRLLT
 Sbjct: 728 ---AEKEWGDGIRGLSLSAARFALLRLEEGPHTKNWRPQLLVLLKLDDELHVKHPRLLT 784

Query: 779 FASQLKGNFLHVKAQKGXTIVGSVIVG-----EALAAEQTIKHVVACGLLENYLMEAE 831
 FASQLK AGKG TIVGSVIVG EALAAEQTIKH LMEAE
 Sbjct: 785 FASQLK-----AGKGLTIVGSVIVGNFLENYGEALAAEQTIKH-----LMEAE 827

Query: 832 KVKGFCQL---AKLREGISH-----GGMKHNTVVLIQSMGWPNGWRQSERVTTDARAW 881
 KVKGFCQL AKLREGISH GGMKHNTVV MGWPNGWRQSE DARAW
 Sbjct: 828 KVKGFCQLVVAAKLREGISHLIQSCGLGGMKHNTVV---MGWPNGWRQSE---DARAW 879

Query: 882 KTFIGTVKNINIDLPFAAHLLVA---SFFPSNVEQFSEG---VWWIVHDGGMLMLL-- 933
 KTFIGTV+ + AAHLALLVA SFFPSNVEQFSEG VWWIVHDGGMLMLL
 Sbjct: 880 KTFIGTVR-VTT---AAHLALLVAKNISFFPSNVEQFSEGNIDVWWIVHDGGMLMLPF 934

Query: 934 -LKQHKVWRK-----TVAQLEDNSISCSIQMK---ATFLYHLRIAEVRIFKDLEVVRT 983
 LKQHKVWRK TVAQLEDNSI QMK ATFLYHLRIAEV EVV
 Sbjct: 935 LLKQHKVWRKCSIRIFTVAQLEDNSI---QMKKDLATFLYHLRIAEV-----EVV-- 982

Query: 984 LEMHDSDISAYTYERHMRLSKMMEQRSQML-----TERDRIAQLVKDRNSMLRLTSIG 1036
 EMHDSDISAYTYER + MMEQRSQML TERDR AQLVKDRNSMLRLTSIG
 Sbjct: 983 -EMHDSDISAYTYERTL---MMEQRSQMLRHMLSKTERDREAQLVKDRNSMLRLTSIG 1037

Query: 1037 SDEDEETETTWTKD KYMAQDLLHTAVYQE KVHM-----SRGQKAKSMEGF---NM 1083
 SDEDEETET YQE KVHM SRGQKAKSMEGF NM
 Sbjct: 1038 SDEDEETET-----YQE KVHM TWTKD KYMASRGQKAKSMEGF QD LNM 1080

Query: 1084 RPDQSNVRRM---KLNEVIVNKSHEAKLVLLNMPGPPRNPEGDENYMEFLEVLT EGLER 1139
 RPDQSNVRRM KLNEVIVNKSHEAKLVLLNMPGPPRNPEGDENYMEFLEVLT EGLER
 Sbjct: 1081 RPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNMPGPPRNPEGDENYMEFLEVLT EGLER 1140

Query: 1140 VLLVRGGGSEVITIYS 1155
 VLLVRGGGSEVITIYS
 Sbjct: 1141 VLLVRGGGSEVITIYS 1156

□>gi|33329256|gb|AAQ10028.1| G K-Cl cotransporter KCC3a-S2 isoform [Homo sapiens]
gi|33329254|gb|AAQ10027.1| G K-Cl cotransporter KCC3a-S1 isoform [Homo sapiens]
 Length = 1091

Score = 2350 bits (5535), Expect = 0.0
 Identities = 868/1303 (66%), Positives = 872/1303 (66%), Gaps = 419/1303 (32%)

Query: 60 MSEMSDPPSDLSQNSGHKKAEGDEYMDTRPGATTSLATVAL----RTSHPQDVIED--- 111
 MSEMS GATTSLATVAL RTSHPQDVIED
 Sbjct: 1 MSEMS-----GATTSLATVALDPPSDRTSHPQDVIEDLSQ 35

Query: 112 --ITGEHSQLLDD---QRNAYLNNNSNYELFE-EESFDKNLA-----KVSSLLNR 154
 ITGEHSQLLDD RNAYLNNNSNYE E +E FDKNL A KVSSLLNR
 Sbjct: 36 NSITGEHSQLLDDGHKKARNAYLNNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNR 93

Query: 155 MANY----QGAKEHEEAENITNLTEGKKPTKTPQMG-----LQNIFGVTFMGVY 201
 MANY QGAKEHEEAENIT EGKKKPTKTPQMG LQNIFGV
 Sbjct: 94 MANYNLTQGAKEHEEAENIT---EGKKKPTKTPQMGTFMGVYLPCLQNI FGV----- 143

Query: 202 ILFLRLLPCTWVVG TAGV LQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRA 261
 ILFLRL TWVVG TAGV LQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRA
 Sbjct: 144 ILFLRL---TWVVG TAGV LQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRA 200

Query: 262 LGPYLGTTFEIFLVYEFGGAVGLCF----AAAMYILGAI----IVPRAAIFHSDDA 309
 LGP EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDA
 Sbjct: 201 LGP-----EFGGAVGLCFYLGTTFAAAMYILGAEIEIFLVYIVPRAAIFHSDDA 248

Query: 310 LKESAAMLNNMRVYGT AFLV LMLV L VVFIGV RYVN KFAS XFLAC VIVS ILAI YAGAI KSSF 369
 LKESAAMLNNMRVYGT AFLV LMLV L VVFIGV RYVN KFAS FLAC VIVS ILAI YAGAI KSSF
 Sbjct: 249 LKESAAMLNNMRVYGT AFLV LMLV L VVFIGV RYVN KFAS LFLAC VIVS ILAI YAGAI KSSF 308

Query: 370 APPHFPVCMLGNRTLSS--IDVCSKTKEINNMTRH VPSK-----NATCDECNS 415
 APPHFPVCMLGNRTLSS IDVCSKTKEINNM VPSK NATCDE
 Sbjct: 309 APPHFPVCMLGNRTLSSRHDVCSKTKEINNM--VPSKLWGFFCNSSQFFNATCDE--- 363

Query: 416 SYFVHNNVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK---SSDVLGSLNHEYVL 471
 YFVHNNV TSIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLGSLNHEYVL
 Sbjct: 364 -YFVHNNV---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVL 419

Query: 472 VDPSAKITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTSLWGFFF 531
 VD ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS F

Sbjct: 420 VD----ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS----F 470
 Query: 532 VYLSNVVLFGACIEGVVLRDKFGVGTLWSWPSFFSTCGAGDAVKGNLV-----PWVIV 583
 VYLSNVVLFGACIEGVVLRDKFG DAVKGNLV PWVIV
 Sbjct: 471 VYLSNVVLFGACIEGVVLRDKFG-----DAVKGNLVVGTLSWPSPWVIV 514
 Query: 584 IGS-----LQSLDNIITGAPPFLRWALLRLQAIK-----VFGHSKANGEPT- 626
 IGS LQSL TGAP RLLQAIK VFGHSKANGEPT
 Sbjct: 515 IGSFFSTCGAGLQSL---TGAP-----RLLQAIAKDNIIPFLRVFGHSKANGEPTW 562
 Query: 627 -----GILIASLDFFLMCYLFLLRLTAALVAPIAELILSM-----C 663
 GILIASLD LVAPI LSM C
 Sbjct: 563 ALLLTAAIAELGILIASLD-----LVAPI---LSMFFLMCYLFVNLC 602
 Query: 664 ALQ-----RYYHWALSFMGMTPNWVNLRPRPRFSICLALMF-----VAM 704
 ALQ RYYHWALSFMG M SICLALMF VAM
 Sbjct: 603 ALQTLRTPNWRPRFRYYHWALSFMG M-----SICLALMFISSSWYYAIVAM 648
 Query: 705 VIAGMIGAEKSSWYYAIYKXIEYQSLSPHTDEDEWDGDGIRGL--AARFALLRLEEGP-- 759
 VIAGM IYK IEYQ E EWGDGIRGL AARFALLRLEEGP
 Sbjct: 649 VIAGM-----IYKYIEYQG----AEKEWDGIRGLSLAARFALLRLEEGPPH 692
 Query: 760 -KNWRPQLLVLLKL-----HPRLLTFA SQLKGNFLHV KAGKGXTIVGSVIVG----- 805
 KNWRPQLLVLLKL HPRLLTFA SQLK AGKG TIVGSVIVG
 Sbjct: 693 TKNWRPQLLVLLKLDEDLHV KHPRLLTFA SQLK-----AGKGLTIVGSVIVGNFLEN Y 745
 Query: 806 -EALAAEQTIKHVVACGLLENYLMEAEKVKGFCQL--AKLREGISH-----GGMKHN 854
 EALAAEQTIKH LMEAEKVKGFCQL AKLREGISH GGMKHN
 Sbjct: 746 GEALAAEQTIKH-----LMEAEKVKGFCQLVVAALKREGISHLIQSCGLGGMKHN 795
 Query: 855 TVVLIQSMGWPNGWRQSERVTTDARAWKTFIGTVKNINIDLPFAAHLLVA---SFFPS 911
 TVV MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPS
 Sbjct: 796 TVV---MGWPNGWRQSE---DARAWKTFIGTVR-VTT---AAHLALLVAKNISFFPS 842
 Query: 912 NVEQFSEG---VWWIVHDGGMMLMLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK 959
 NVEQFSEG VWWIVHDGGMMLMLL LKQHKVWRK TVAQLEDNSI QMK
 Sbjct: 843 NVEQFSEGNIDVWWIVHDGGMMLLPFLLKQHKVWRKCSIRIFTVAQLEDNSI---QMK 898
 Query: 960 ---ATFLYHLRIAEV RIFK DLEV VRTLEMHDSDISAYTYERHMRLSKMMEQRSQL--- 1013
 ATFLYHLRIAEV EVV EMHDSDISAYTYER + MMEQRSQL
 Sbjct: 899 KDLATEFLYHLRIAEV-----EVV---EMHDSDISAYTYERTL---MMEQRSQLRH M 945
 Query: 1014 ----TERDRIAQLVKDRNSMLRLTSIGSDEDEETETTWTKD KYMAQDLLHTAVYQE KVHM 1069
 TERDR AQLVKDRNSMLRLTSIGSDEDEETET YQE KVHM
 Sbjct: 946 RLSKTERDREAQLVKDRNSMLRLTSIGSDEDEETET-----YQE KVHM 988
 Query: 1070 -----SRGQKAKSMEGF---NMRPDQSNVRRM---KLNEVIVNKSHEAKLVLLN 1112
 SRGQKAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLN
 Sbjct: 989 TWTKD KYMASRGQKAKSMEGF QD L NMRPDQSNVRRM HTAVKLNEVIVNKSHEAKLVLLN 1048
 Query: 1113 MPGPPRNPEGDENYMEFLEVTEGLERVLLVRGGGSEVITIYS 1155
 MPGPPRNPEGDENYMEFLEVTEGLERVLLVRGGGSEVITIYS
 Sbjct: 1049 MPGPPRNPEGDENYMEFLEVTEGLERVLLVRGGGSEVITIYS 1091

 >gi|38565928|gb|AAH62099.1| Unknown (protein for MGC:69652) [Mus musculus]
 Length = 1106

Score = 2345 bits (5523), Expect = 0.0

Identities = 868/1326 (65%), Positives = 884/1326 (66%), Gaps = 422/1326 (31%)

Query: 1 MHPETTTKMASVRFMVTPTKIDDIPGLSDTSPDXSSRSSSRVFSSRESPETSRSEPM 60
 MHPPE TTKM+SVRFMVTPTKIDDIPGLSDTSPD SSRSSSRVFSSRESPETSRSEPM
 Sbjct: 1 MHPPEATTKMSVRFMVTPTKIDDIPGLSDTSPDLSSRSSRVRFSSRESPETSRSEPM 60

Query: 61 SEMSDPPSDLSQNSGHKKAEGDEYMDTRPGATTSLATVAL-----RTSHPQDVIEDITGE 115
 SE+S GATTSLATVAL RTS+PQDV ED
 Sbjct: 61 SELS-----GATTSLATVALDPSSDRTSNPQDVTED--- 91

Query: 116 HSQLLDDQ---RNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRMANY--- 158
 D RNAYLNNSNYE E +E FDKNLA KVSSLLNRMANY
 Sbjct: 92 -----DGHKKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRMANYTNL 144

Query: 159 -QGAKEHEEAENITNLTEGKKPKTPQMG-----LQNIFGVTFMGVYILFLRL 208
 QGAKEHEEAENIT EGKKPKTP+PQMG LQNIFGV ILFLRL
 Sbjct: 145 TQGAKEHEEAENIT---EGKKPKTKSPQMGTFMGVYLPCLQNIFGV-----ILFLRL- 193

Query: 209 PCTWVVGTTAGVLQAFIAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLGT 268
 TWVVGTTAG+LQAFIAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP
 Sbjct: 194 --TWVVGTTAGILQAFIAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP--- 247

Query: 269 TFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDALKESAAM 316
 EFGGAVGLCF AAAMYILGAI IVPRAAIF SDDALKESAAM
 Sbjct: 248 -----EFGGAVGLCFYLGTTFAAAMYILGAIIEIFLVYIVPRAAIFRSDDALKESAAM 299

Query: 317 LNNMRVYGTAFLVLVLMVLVVFIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFAPPHPV 376
 LNNMRVYGTAFLVLVLMVLVVFIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFAPPHPV
 Sbjct: 300 LNNMRVYGTAFLVLVLMVLVVFIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFAPPHPV 359

Query: 377 CMLGNRTLSS--IDVCSKTKEINNMTRHVP SK-----NATCDECNSSYFVHN 422
 CMLGNRTLSS +D+CSKTKE++NMT VPSK NATCDE YFVHN
 Sbjct: 360 CMLGNRTLSSRHLDCSKTKEVDNMT--VPSKLWGFFCNSSQFFNATCDE---YFVHN 413

Query: 423 VQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK----SSDVLGSLNHEYVLVDPSAKI 478
 V SIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLG+LNHEYVL D I
 Sbjct: 414 V---ISIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGNLNHEYVIAD---I 466

Query: 479 TTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTSLWGFFFVYLSNV 538
 TTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS FVYLSNV
 Sbjct: 467 TTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS----FVYLSNV 521

Query: 539 LFGACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIVIGS--- 586
 LFGACIEGVVLRDKFG DAVKGNLV PWVIVIGS
 Sbjct: 522 LFGACIEGVVLRDKFG-----DAVKGNLVGTL SWPSPWVIVIGSFFST 565

Query: 587 ----LQSLDMIITGAPPFLRWALLRLLQAIAK-----VFGHSKANGEPT----- 626
 LQSL TGAP RLLQAIAK VFGHSKANGEPT
 Sbjct: 566 CGAGLQSL---TGAP-----RLLQAIAKDNIIPFLRVFGHSKANGEPTWALLTAA 613

Query: 627 ----GILIASLDFFLMCYLFLLRLTAALVAPIAELILSM-----CALQ--- 666
 GILIASLD LVAPI LSM CALQ
 Sbjct: 614 IAELGILIASLD-----LVAPI-----LSMFFLMCYLFVNLACALQTLLR 653

Query: 667 -----RYYHWALSFMGMTPNWVNLRPRPRFSICLALMF-----VAMVIAGMIG 711
 RYYHWALSFMGM SICLALMF VAMVIAGM
 Sbjct: 654 TPNWRPRFRYYHWALSFMGM-----SICLALMFISSWYYAIVAMVIAGM-- 697

Query: 712 AEKSSWYYAIYKXIEYQSLSPHTDEDEWDGIRGL---AARFALLRLEEGP---KNWRPQ 765
 IYK IEYQ E EWGDGIRGL AARFALLRLEEGP KNWRPQ